

1342						
CACCTTGACT	TGGGTGAGTA	GGCACGGTAG	GAGCTTTCT	CATAATCTCC	TCTACCGTTG	360
ACAAGGAATC	AGCCATGAGT	TCTTCAGTTG	AAGGTTCACT	TGCAGGAGTG	CGAACTACTG	420
CCTCATCTTC	TTTCAGAACT	TCATCATAGC	CTTTTACTTT	TTCTAAATCT	CTCAGAACTCT	480
GCTCTTAA	GCGTAATTTC	TCTTCTGCTC	TTGACTTTTC	ACTCAAAAGT	TTTTCCCTCCT	540
TGTTGAGAAT	CCATAATATT	AGAGCTGAGA	AGTCCAAAAA	AAGCAATCTA	TGATACTTTT	600
CCTAACGGAT	TTTGTCACTT	CCAGACCAT	ATCATAACCAT	GTTTCCCTG	CAAAGGTTGA	660
CTGGGAA						667

(2) INFORMATION FOR SEQ ID NO: 315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1483 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

GGGAAGCCAA	GGTATTTAT	CGGATGAAAGT	TGTTACTAGT	TCTTCACCGA	TGGCTACAAA	60
AGAGTCTTCT	AATGCAATTA	CTAATGATTT	AGATAATTCA	CCAACTGTTA	ATCAGAAATCG	120
TTCTGCTGAA	ATGATTGCCT	CTAATTCAAC	CACTAATGGT	TTAGATAATT	CGTTAAGTGT	180
TAATAGTATC	AGCTCTAATG	GTACTATTG	TTCCAATTCA	CAATTAGACA	ACAGAACAGT	240
TGAATCTACA	GTAACATCTA	CTAATGAAAA	TAAGAGTTAT	AAGGAAGATG	TTATAAGTGA	300
CAGAATTATC	AAAAAAAAGAT	TTGAAGATAC	TGCTTTAAGT	GTAAAAAGATT	ATGGTGCGGT	360
AGGTGATGGG	ATTCATGATG	ATCGACAAGC	AATTCAAGAT	GCAATAGATG	CTGCAGCTCA	420
AGGGCTAGGT	GGAGGAAATG	TATATTTCC	TGAAGGAAC	TATTTAGTAA	AAGAAATTGT	480
TTTTTTAAAA	AGTCATACAC	ACTTGAATT	GAATGAGAAA	GCTACAATT	AAATGGTAT	540
AAATATTAAG	AATCACCCCTT	CCATTGTTT	TATGACAGGT	TTATTTACGG	ATGATGGTGC	600
GCAAGTAGAA	TGGGGCCCAA	CAGAAGATAT	TAGTTATTCT	GGTGGTACGA	TTGATATGAA	660
CGGTGCTTG	AATGAAGAAG	GAACCTAAAGC	AAAAAACTCA	CCACTTATAA	ATTCTTCAGG	720
TGCATTGCT	ATTGGGAATT	CAAATAACGT	AACTATAAAA	AATGTAACAT	TCAAGGATAG	780
TTATCAAGGG	CATGCTATTC	AAATTGCAGG	TTGAAAAAT	GTATTAGTTG	ATAATTCTCG	840
TTTTCTTGGG	CAAGCCTTAC	CCAAACCGAT	GAAGGATGGG	CAAATCATAA	GTAAGGAGAG	900
CATTCAGATT	GAACCATTAA	CTAGAAAAGG	TTTCCTTAT	GCCTTGAATG	ATGATGGGAA	960
AAAATCTGAA	AATGTGACTA	TTCAAAATTC	CTATTTGGC	AAAAGTGATA	AATCTGGGAA	1020

1343

ATTAGTAACA GCAATTGGCA CACACTATCA AACATTGTCG ACACAGAACCC	1080
TAAATTCAA AATAATCATT TTGATAACAT GATGTATGCA GGTGTACGTT TTACAGGATT	1140
CACTGATGTA TTAATCAAAG GAAATCGCTT TGATAAGAAA GTTAAAGGAG AGAGTGTACA	1200
TTATCGAGAA AGCGGAGCAG CTTTAGTAA TGCTTATAGC TATAAAAACA CTAAAGACCT	1260
ATTAGATTAA AATAAACAGG TGTTATCGC CGAAAATATA TTTAATATTG CCGATCCTAA	1320
AACAAAAGCG ATACGAGTTG CAAAAGATAG TGCAGAaTwT TTAGGAAAAG TATCAGATAT	1380
TACTGTAACA AAAATGTA TTAATAATAA TTCTAAGGAA ACAGAACAAAC CAAATATTGA	1440
ATTATTACGA GTTAGTGATA ATTTAGTAGT CTCAGAGAAT AGT	1483

(2) INFORMATION FOR SEQ ID NO: 316:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2453 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

CCTGAACGCT TTTTTATAAA TATCATAAAG CCAATCTGAT TTATCAAGTG TGTCTAACCG	60
ACCGGAATTA AAATTCAATTG CATACTCCAT CGCTTCTAAA AACTCAATT TTGAAAAGAC	120
GTTAAATCA TCTAAATTCT GACTCCAATA TAATAACAAA ACCAATCCC TAATATCCTC	180
TGGTTGATTA TTCAATAAT TTAAGTTGGT TTCATAAAAC CCTGGAGTTC CAAATAGAGG	240
CAACTTTTT TCTTCAATTG GAGTTCTTT CCTTAGGGCA TGCTCAAAGT CTATAATATA	300
AATATTATTT CTATTATCAA TAAGTATATT ATTAATGAT AAATCTCTAT AGGAAAGATT	360
ATATTGGAG TTTATTATCT CCATATAATC ATTAATGTT AAAACCAAT CATAcgAGCC	420
ACTAACCCATA TTATACTCGC TTAATTATC TGCAATAATA AACTCAAATT CCACAAAATA	480
CGAATTCTTT ATGTTAAAT CGTTAAAAC TTTGGAGTA AATTCCTCCT TTTCCAATTC	540
TACTAATATT TCTCTTTCAT TTATTAACG ATTACAGAA TCTCTATTG TAAAATCAAC	600
CAACGATAAA TCACTAGCTT CTTTAATAAA AGAATAAACT CGCTTTGAG TATTAATAC	660
TTTATAAACT CCACCTTGG CATTTTAGA AATCACTTCC AAAATAATAT ATTGATCAGG	720
AATAGTGTAA TATCTTGAA TATAGTAATC CCTTATTGGA ACATTCACT TTGAAGGGAT	780
TTTCTTATCT CTTTATCCT TGAAAGTGT ATCTTTACG AACTCCCCAT ATCTGTAATA	840
TACAACCTCG CTAAGTGAA ATCTGAAATC TGATGGTATG TTTACACCCCT TTACACCTTT	900

ATACAATATT TCTAATTGTT	1344	GTAACAAACG TTGAACTCT TTATTATCTT TTGGATAAAAT	960
TGTAATGAAT TTCCCGACTT		GTGAATAACC ATTAAGCCCT GTATTTGCA AAGAAAGTTC	1020
TTTAATGCTA ACCAAAATTT		TGAAATTATCTT CTTCTTCTCT CTAGAAAATA TAAAATCAA	1080
GAATTTTTA GCAACCAAAT		TAGCATTAA TATTGAAGCG CTCAGGTGTA TTTTAAATCC	1140
CTTAGATTGG GTGATATTAG		ACGGCAAATT ATATAACCA TGTTCATCAC TAAAATTATC	1200
ACTAATTTTA TATTCTAATA		ATAAATTATG GTATGCGTCT TCTATTTCAG TTTCATAGTC	1260
CAAATAGTTT AAATACTTTT		CGTAATTCTAT ATTAAGAAAT CTTCTCCATA AATTTTTAGA	1320
CCATCATTAA AAGCCAAACA		ATTTAAAGCG TGATAATAAA TGTTGATAAT CAATGTAAC	1380
TTCAGTCCTC TATTTTGTAA		TTCCCTTCACC ATAATTTTA TGCTATATCT ATTTTCTCGA	1440
GGCAATTAT AGGACTTCAA		GATAAAACCA TAAAAGAGAT AAGTATTATA ATCTGACAAT	1500
CCAGTTTCAG AATAATTTT		TAGAAAAATA TCTAGTGATT CTGATAATTCA ATCCGGAATA	1560
ATTCTTTAA CATCGTATT		ATTTTTCATA TCGGCCACTC TTCCCTAAAA AGCTCACAAAT	1620
AAAATTTAA ATTTCTATAC		ACAATCCGA GAGTAGTCTC ACAATTGAA CATTTCACAT	1680
CACTCTTAAT ATATAAAAAA		TGAATTAAATC AGAAACCTCT GACTAAGATT TCCTAATTAA	1740
TTCACTTTCT ATATCATAGT		AAGGAATTCT ATTATCCCTA ATTGAAAATT GAAATTTAT	1800
GTTTTATATA TTAACAATTA		TGCGGATTGT AAATCTTGTC TAACAAAATG GCAAGTGCTA	1860
CTATGTGCC CAGAAGGCGA		TGCAACGCTA TTTTGAATTG AAAGAGCATA ATCATCCATA	1920
TCATTTAAGT CACGGATTAG		CAATGCTTCC TTCTCTCTC CGACAATTCC AAATTTCTA	1980
ATTACCTTTT CAGGATTATC		AAAAAATTCT CCAACAACCTT CCATATTTC TTGAAGTTCA	2040
TTCAAGAAAG CTTTCATTTG		ACTACTCATT ATATAGCTCC TTTTCTATTA CTTTATTTGG	2100
AATCAAAACT TACTTGTACA		TTGAAACAC CTCTATTCTA CGCTTTCATA TTGCTGCATG	2160
ACACTTTCAA AATCAAATTG		CTAAAAATAA TTTTTAAAG CTTAATTCTAG ATTTAATTAC	2220
ATATATCTCA AAAAATTGTT		TTGAAATTAG TAAATTAAA TAGGTTCTG TACTTATAGG	2280
AACTAGTTAT AAAAATTTCG		CCCATCATAA AATATCTATT TAAGTAAAAC AAAAATTAA	2340
TAATTTTTG ATTTTAAGT		GACTATAATC TCCTATCTAT AAATACCATT CGCAGGACCT	2400
GGATCAATCC CTCTAGCCAT		CTTATGAACT TGAGTTCCCTC CAGACAGTCC CGG	2453

(2) INFORMATION FOR SEQ ID NO: 317:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1049 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

CCAATTGAA GGCTCTAAAA CAATGGAAAA GTGCTACACA GATGTGACAG AATTTGCCAT	60
TCCAGCAGTA CTCAAAAACT TTACTTATCA CCAGTTTAG ATGGCTTTAA CAGCGAAATT	120
ATTGCTTTA ATCTTCTTG TTGCCTAAT TTAGAATAAG TACAAACAAT GTTGGAACAG	180
GCATTCAAAG AGAACGACTA TGAGAACATCG ATTCTCCATA GTGACCAAGG CTGGCAATAC	240
CAACACGATT CTTATCATCG GTTCCTAGAG AGTAAGGGAA TTCAAGCATC CATGTCACCG	300
AAGGGCAACA GCCCAGACAA CGGCATGATG GAATCTTCTT TTGGCATTAA GAAATCGGAG	360
ATGTTTATG GTTATGAGAA GAACTTTAGA TCTTTAGAAA ACCTTGAACA AGCTATTGTG	420
GACTACATTG ATTATTACAA CAACAAGAGA ATTAAGGTA AGCTAAAAGG ACTTAGCCCT	480
GTGCAATACA GAACTAAATC CTTCCGATAA ATTAATTGTC TAACTTTGG GGTGCAGTAC	540
ATTTTGGTA TATATAAAAT TTGTAGGAGC TATATCTACA ATTTTATATT CCCAGTTTAT	600
GGATGTAACT TACTATATTC ACAATGTTAT CCAGTGTGTT TTCTCTAATA TTTAAGGAGT	660
GTTCTGTTTC TCGAATAAAAT TCTTCAAAGT TTAACCCGTC AACTTGTCC TGAACAAGAA	720
AATAATCATC CACGATATAA AATTATCATCAG TTAATTAGT AGTATAACTT TTATCGGCTA	780
ATTTTTTAG CATGTGAGCT TCATTTTTTA TATCATCAG AGCTGTCCAT TCTCCCTTCAG	840
CATCATAATT CACAAAAGGT CTTGACTGCT TGATGATTAC TTTTGCCCG TCCGATTTTC	900
TAATTGCCCG ATAAACATTT CCTTTATTG ATCTCTTAAT AATTTTTCC ATTTTGTATT	960
TATTTATTGC AGAGTCCCTA CTTGAAACTT CACATGTGGT TTGAAAATAA ATCCTTTTT	1020
CTTCTCTGA AAATAAAATCC ATTTTCCGG	1049

(2) INFORMATION FOR SEQ ID NO: 318:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 776 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

TTAGTTGGTT AGAACAGAA AATCGCCGAA GTGGTTATTT ATTTTTGAAT AAATTTAACG	60
AACCAATTAC AGCAAGAGGA GTTGCTAAC AGTTAAAAAA TTATGCTGAT AAATACAAAA	120
TGAATCCTAA AGTAATTAC CCTCATTCTT TTAGGCATTT ATTTGCTAAG AATTTTTAG	180

1346	
CGAAGTATAA TGATAATTGCC TTGCTTGCAG ATTTGATGGG ACACGAAAGT ATAGAAACTA	240
CTCGAATTAA TCTAAGGAAA ACAGCTACTG AACAAACAAA TATTGTAGAT AAAATTGTTA	300
ATTGGTAAAAA AATAACAGGT GGTCAAACGT ACTACCTGCT ATTTTTGTGA TTATGGCTCT	360
TATTATGGGA ATATACTTAT GAATTGGGTT GTTATAAAAAA TAAAAGATAT TTTTCAATA	420
AATAACAGGTC TTTCTTACAA GAAGGGCGAT TTAAGCATT AATAATAAGG TGTTAGAATT	480
ATACGTGGTG GTAATATTAA GCCTTTAGAA TTTTCTCTGT TGGATAATGA TTACTACATT	540
GATACACAAT TCATCTCCTC TGAGCAAGTT TATTAAAC ATAATCAGCT AATAACACCT	600
GTATCAACCT CTTAGAACAA TATTGGAAAG TTTGCAAGAA TCGAGAAAGA CTATGATGGT	660
GTTGTGGCTG GTGGATGTAT TTTCAATTAA ACACCATTG AAAGTGCAGA GATGATGTCA	720
AAATGTCTAT TATGTAACCTT GTCCTCTCCG TTATTTATA AACAATTGAA AGCAAT	776

(2) INFORMATION FOR SEQ ID NO: 319:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 658 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

TGCAATGCGG CGGCTGCATA CGCTTGATCC GGCTACCTGC CCATTCGACC ACCAAGCGAA	60
ACATCCATC GAGCGAGCAC GTACTCGGAT GGAAGCCGGT CTTGTCGATC AGGATGATCT	120
GGACGAAGAG CATCAGGGC TCGCGCCACC GAACTGTTCG CCAGGCTCAA GGCGCGCATG	180
CCCGACGGCG AGGATCTCGT CGTGACCCAT GGCGATGCCT GCTTGCCGAA TATCATGGTG	240
GAAAATGGCC GCTTTCTGG ATTCAATCGAC TGTGGCCGGC TGGGTGTGGC GGACCGCTAT	300
CAGGACATAG CGTTGGCTAC CGGTGATATT GCTGAAGAGC TTGGCGGCGA ATGGGCTGAC	360
CGCTTCTCG TGCTTTACGG TATCGCCGCT CCCGATTGCG AGCGCATCGC CTTCTATCGC	420
CTTCTTGACG AGTTCTTCTG AGCGGGACTC TGGGGTTCGA TGTGACAGC CCGCTTAATG	480
AGCGGGCTTT TTTTCTCTGA GGCTGGACGA CCTCGCGGAG TTCTACCGGC AGTGCAAATC	540
CGTCGGCATC CAGGAAACCA GCAGCGGCTA TCCGCGCATC CATGCCCG AACTGCAGGA	600
GTGGGGAGGC ACGATGGCCG CTTTGGTCCC GGATCAATTG CGCGACCGG ATCGATCC	658

(2) INFORMATION FOR SEQ ID NO: 320:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1475 base pairs
 - (B) TYPE: nucleic acid

1347

(C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

CCGGCTTAAT	TTTTAGAAAA	CGTGGGCAGG	GAACCTTGT	TCTCTCTCGT	GGCAGCTCAA	60
AAAGAAAAATT	AATCGTTCCA	GAAAGAGATA	TCCGGGGACT	GACAAAATA	TCTGAAGATG	120
CTCATTCTAC	AATTGACTCG	AGGATTATTC	ACTTCAAATT	AGAATTGCA	AATGAATT	180
TAGCAGAAAA	ACTACAGGTC	GCTTGCAGA	GTCCAGTTA	TAATATTTAC	CGCCTGCGTA	240
TTATTGACGG	TAAACCTTAT	GTTCTGGAAC	AAACTTATAT	GAGTACCGAT	CTTATTCCAG	300
GTATTACTGA	AGATATTTA	CAAAAATCGA	TTTACAATTA	CATTGAAGGA	AAGTTAGGAT	360
TGCATATTGC	CAGTGCTACA	AAAATCTTAC	GAGCTTCTTC	TAGTTCAGAA	AATGAGAAC	420
ATTACTTGCA	GCTCCTTCCA	ACGGAACCGG	TATTTGAAGT	AGAACAAAGTG	GCTTATTG	480
ATAACGGAAC	TCCGTTGAG	TACTCGATTA	GTGCGTACCG	CTATGATT	TTTGAATT	540
ATTCTTTGC	ATTACGACAT	TCCTCCTAGG	AGAAAATGTG	AAAATGAAGC	CAATCTT	600
CAGACTCTAG	TTTAAGAAAA	ATTAAAACA	GGGCAAGAAG	GTCCCACATCA	TGCTTAAATG	660
GTTTCTCTT	TCTAAATAAG	ATGGCTTAA	AAAGAGTGT	GTTGTATCCA	TCATGTTGAA	720
AAATATCTTC	GTATAGCTTA	TACACTAGGT	ACTGAAATTG	TTCACCTGAT	CTACTT	780
TAGTTATTTA	GTTTAAATA	GTGTTCAAA	CATTCTAC	CTGACGAGAA	GTTTTGAGT	840
CTTTTCTTGT	AACACATATA	GTATACGTG	GTTAGAATAG	TAGACTGTGA	CTTCTAACAA	900
ATTGCTAGAA	ATGAATTCA	ATCTCCAAT	TTATTTGTC	ATATCTCTT	TTAATATATT	960
AAATAAATT	AAATCATAA	TCATTTAAA	AAATTTATT	TTTTATTTT	CATTACGAAT	1020
AAATATAGATG	AAGGGAAAG	AGTATGAAA	CAGAACTGT	TCTTTGCTA	TTAGTTCAA	1080
AGGAGAAAAA	ATGAAAGTAG	AAAATATTTC	GTATAGGTG	GATCATCGTA	AATTGTTGA	1140
TAATATTCT	TTTGACTACT	CGAGTTCAGA	CGTGACATTA	ATTACTGGTA	AAAATGGTAC	1200
AGGAAAGTCA	ACTTTACTAT	AGTAGATTGA	AACTAGAATA	GTACACATCT	ACTTCTAAA	1260
TATTGTTAGA	AATCGATTG	ACTATCCTGA	TCTATTTGTC	CTGTTCTTAT	TTCATTTCAC	1320
TATATCTCAA	ATTGAGTATG	ACGAAGTGCG	CTCCCATGTC	CTGGGAACGC	ACTTTCTTCA	1380
TATTTTCAT	ATTCTGAAAT	CCATCGATAA	AGACTATTGG	GATGAATT	TAAAGTTGAA	1440
CTAATCATTT	TTACAGGATG	AGATTTACAG	CAGAG			1475

(2) INFORMATION FOR SEQ ID NO: 321:

1348

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 560 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

GAATATATA TACTTCATCT TAATAGTGAG CAAGCTAAAC TTAGCATTTTC ATGCCCTCAT	60
ATGGGATGTT CTTTGACTAA ATAATATGAT TATCGAGATA TATCTGGATA AATGAACTAA	120
TAAGTCTGAC GCGTAGACTT ATCAAAGTCA TTGGCATAACA CCACTATGAA CTCGTTGGTC	180
TGTTCAAATC CCAACACATT ACCTGAGAAG AAAGTTGCAA TGTTGTTTT GGTGCGGGTT	240
TGAATTAAA AAATTGTTA TGAGTACCT AATCTAAGGA ATTAGAACAA TGCCCTAAT	300
TTTTCTTTAA TACACTGAAA CATTGATGAT TCTGGCTGTA TTTTGAAAC AGCTCTTCTT	360
TGCTCCTGGA AAATATCTTC AGAAGTTATA TTCTCTATTTC CTAACGCTAC TTGAGTTTT	420
TTTCTAAAAT ATTCTTTCC GTGCCATCT TTAGAAAAAT CATAACCTTC CCTATCTACG	480
CTGTTACACA AATTAGCTAA AAAarACTCT GGGGTTGGGA AAGGAAGATA AGAAaCGTAT	540
TTAGCCCCATA ATCTATAAAG	560

(2) INFORMATION FOR SEQ ID NO: 322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 643 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

CCGCCCCGCC ACCGCTGCCT ATCCCTGGGA GAGGGTCACC TGGAGTGAAC CTAGAACGAT	60
AGACACGGTG CGGTACGACC TCGTACTACT TTGCGCGACG GCCTCGTCCG TTGTCATCCA	120
CGAACTGATC GGACATGGGT GCGAACACTT CAGAGAAAAA ATCGTTGGAC TGCGTGTGG	180
GCCTGAGGAA CTACGGGTGG TGGCTTTCC GAAGAACGGC TCCGGTTTG ATGACGAGGG	240
TACACCTCC GAAGAGATTG TACTTGTGGA GAACGGCATT GTGAGGCACG CTGTCAGGGA	300
TGGGGCACT GGAGGAATGG CGCCTTTTC CGTTTGACC AAAGTGGCAT CACATGGTGT	360
CAAACCTGGC TCAAGATGTA CGCATCTCAA GGCGGAAGGG GAATCGTCAC AGGAAGGGAGT	420
TACCGGAGTA CCCGCCAAC GCACCGTTG GATAGAGCAT TTTCTGCAG CGAACTACCA	480
TTCAGGTGCA GCCTTTTCA GGTCTGGCCT TGCCTGGTA GGCAGCCGAG AAGAACTCTT	540

1349

ATATCCCTTA ATGCCTTCAGCATGCAAT TGATATCTAC GAACTGGCCA GCTTATTGTG	600
GCATTTAGAC GGTCAACCGG AACGAGCACG TAGGGTACTG TGC	643

(2) INFORMATION FOR SEQ ID NO: 323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 780 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

GGTACCCACT CATTCTTGAT GAATTGTGAA CAGTTGCCCT TGGGTCGTTT TGCGAGTTGA	60
AGTCAAGAAG AGGAAAAAAA CAAAAAGGAG AAATACTCAT GGCAGTAATT TCAATGAAAC	120
AACCTCTTGA GGCTGGTGTAA CACTTGGTC ACCAAACTCG TCGCTGGAAT CCTAAGATGG	180
CTAAGTACAT CTTTACTGAA CGTAACGGAA TCCACGTTAT CGACTTGCAA CAAACTGTAA	240
AATACGCTGA CCAAGCATAAC GACTTCATGC GTGATGCAGC AGCTAACGAT GCAGTTGTAT	300
TGTTCGTTGG TACTAAGAAA CAAGCAGCTG ATGCAGTTGC TGAAGAAGCA GTACGTTCA	360
GTCAATACTT CATCAACCAC CGTTGGTTGG GTGGAACTCT TACAAACTGG GGAACAATCC	420
AAAAACGTAT CGCTCGTTG AAAGAAATTAA AACGTATGGA AGAACATGGA ACTTTGAAAG	480
TTCTTCCTAA GAAAGAAGTT GCACTTCTTA ACAACAAACG TCGCGTCTT GAAAAATTCT	540
TGGGCGGTAT CGAAGATATG CCTCGTATCC CAGATGTGAT GTACGTAATG ACCCACATAA	600
AGAGCAAATC GCTGTTAAAG AAGCTAAAAA ATTGGGAATC CCAGTTGTAG CGATGGTTGA	660
CACCAATACT GATCCAGATG ATATCGATGT AATCATCCCA GCTAACGATG ACGCTATCCG	720
TGCTGTTAAA TTGATCACAG CTAAATTGGC TGACGCTATT ATCGAAGGAC GTCAAGGTGT	780

(2) INFORMATION FOR SEQ ID NO: 324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 624 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

CGGGAAAAAT CAGATTGTGG GTTCAGATAT CGAATTAGCC AAGGCTATCG CAACAAAAC	60
AGGTGTCGAA TTGGAACTAT CTCCCATGAG TTTGATAAT GTACTGGCTA GTGTTCAATC	120

AGGAAAAGCC GACCTTGCCA TATCAGGTGT TTCTAAGACA GATGAACGGA GCAAGGTGTT	1350 180
TGACTTTCC ATTCCCTACT ATACTGCAAA AAATAAAACTC ATTGTCAAAA AATCTGACTT	240
GACTXACTTAT CAGCTGTAA ACGACTTGGC GCAGAAAAAG GTTGGAGCGC AGAAAGGTC	300
GATTCAAGAG ACGATGGCGA AAGATTGCT ACAAAATTCT TCCCTCGTAT CTCTGCCTAA	360
AAATGGAAT TTAATCACAG ATTAAAATC AGGACAAGTG GATGCCGTTA TCTTGAAAGA	420
ACCTGTTCC AAGGGATTG TGAAAATAA TCCTGATTAA GCAATCGCAG ACCTCAATT	480
TGAAAAAGAG CAAGATGATT CCTACGCGGT AGCCATgAAA AAAGATAGCA AGAAATTGAA	540
AGAGGCAGTT CGATAAAACC ATTCAAAAGT TGAAGGAGTC TGGGAATTAA GACAAACTCA	600
TTGAGGAAGC CTTATAAGCA TCCA	624

(2) INFORMATION FOR SEQ ID NO: 325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

TCTTATGAAG CCGAACGCGT ATTATGGCG GATAGGTTG GTCTGCAGAA ACTGACAAAT	60
CTAGTCCAT CAGCGTATAT GGAATCTnTG GCTGAGAAC AGTCCCAGGG TGAAC TGACT	120
TATGAGCAGG TTTATGAGGA TGCAACGGCT TATCATCATA CCATTGATGC GAGTACAGAG	180
GAGGCAGACT TGGTTCTCT ACGTATTGTA GAACTATTGT CTCGAAGAGG CTTTAGCTTC	240
AGTCCTGCGA TCTTACTTGC TATTCTAAAG GAGTTGTTTC AAGATATATT TGAACCCCTCG	300
ATTCCGGTAG GTCAATTTCG TCAGACTAAT ATCACAAAGA ATGAACCTGT TTTGAATGGT	360
GAAAGTGTG TGTACTCTGA TTACTCCATG ATTCAAATGA CCTTGGATTA TGATTTAAAT	420
CAGGAAAAAC AAGTTGCATA TGCGACACTA ACCCAGGCGG ATATGGTTAA AAAAATCCAG	480
CATTTTATTT CAGGAATCTG GCAGATTCTG CCATTTCGCG AAGGAAACAC TCGGACGGTA	540
ACGGTATTT TGATTCAGTA TCTTCGTGAG TTTGGTTTG ATATTGATAA TACACCATT	600
CAGCAACATT CCAAGTATTT TCGTGATGCC TTAGTGTAG ATAATGCAAA GATTTTACAG	660
CGACGCTCTG AGTTTTAAC AGCTTTTTT GAAAATCTCT TGCTCGGTGG TCAAAATGAT	720
TTGTCTTCAG AAAAATGTA TCTAGATTAA GACCTCGATC TTTCATAATC CTAATACTGA	780
GTAAACATTG AATTTAGGA AAAAATGAAG TAAATATTCT CACAAGAAAA CGTATATCAT	840
CAAAGTTGG CTCTTGTCA ATTGTAGTGG GTTGAAGAAA AGCTAAGTTC GAGAAAGGGC	900

1351

AAATTCGGC CTTCCCTTT TGATGTTAG AGCGATAAAA ATCCGGTTTT TTGAAGTTT	960
CAAAGTTTCG AAAACCAAAG GCATTGCGCT TGATAAGTTT GATGAGATTA TTGGGCGCTT	1020
CCAGTTGGC ATTAGAATAG TGAGTTGAA GGGCGTTGAT AACCTTTCT TTATCTTGA	1080
GGAAGGGTT AAAGACAGTC TGAAAATAG GATGAACCTG CTTAAGATTG TCCTCGATAA	1140
GTTCGAAAAA TTTCTCCGGG TCCTTATTCT GAAAGTGAAA CAGCAAGAGT TTGAAGAGCC	1200
GATAGTGATG TATCAAGTCT TGTGAATAGC TCAAAAG	1237

(2) INFORMATION FOR SEQ ID NO: 326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

TTTGATTTT CTGAATTAGA AGAGATTGAA TTGCCTGCAT CTCTAGAATA TATGGAAACA	60
AGTGCATTTT CTTTAGTCA AAAATTGAAA AAGCTAACCT TTTCCTCAAG TTCAAAATTA	120
GAATTAATAT CACATGAGGC TTTTGCTAAT TTATCAAATT TAGAGAAACT AACATTACCA	180
AAATCGGTTA AAACATTAGG AAGTAATCTA TTTAGACTCA CTACTAGCTT AAAACATGTT	240
GATGTTGAAG AAGGAAATGA ATCGTTGCC TCAGTTGATG GTGTTTGTT TTCAAAAGAT	300
AAAACCAAT TAATTATTA TCCAAGTCAA AAAATGACG AAAGTTATAA AACGCCTAAG	360
GAGACAAAAG AACTTGATC ATATTCGTTT AATAAAAATT CTTACTTGAA AAAACTCGAA	420
TTGAATGAAG GTTTAGAAAA AATCGGTACT TTGCAATTG C	461

(2) INFORMATION FOR SEQ ID NO: 327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1436 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

TAACATTTAG GTACCTCTTC TTAACAAAGT TCAATAGTAA CAATTAATAT TTTAAACAAT	60
ATATCAAACA TCAATGACTA GAATACTTGCA ATCATCCTTC TTTCCATAGA TTGGATCAAT	120
AGCAGAAGAA TTAAATCTCA TCTTAATTAA CTCTCAAAA GTTTTATTTT GATTATTTG	180

1352	
ATAGAATTCA TAAAAGCCAT CGCTCATTAA AACAAATTGT TCACTAGTAA CATCTATTG	240
ATTAATAATA GCATGGCTA AAAATCTCTC ATCCAACGAA CCTATCCAGT ACCCACTCGG	300
TTGATTTAGAT AATTTCTGA TTTTTGTAA ATAATTTTT TTATTTAAA CACTATTTGT	360
ACCAATTGAA TCTTTATCT CATTTCCTCC TTTTCAAAT AAGTTATCTA CTCTATGATC	420
AGTTATTCCTCC ATTCGTTA CTAACATGAC GCAGTCACCT AGCATCATAT ACTCCAACCT	480
TTTTCTGAA AGTTAGCAA ATATTGGTAA GCGATAATAT AGTATATTGA AACTAGAATA	540
GTACACCTCT ACTTCTAAAA CATTGTTAGA AATCGATTG ACTGTCCTGA TTGATTTGTC	600
CTATTATTAT TTCATTTTAC TATACTCTGT TAATTATAT GAGTTAAAC CGATTCATC	660
TTAACCTCG AGTAAAGCAG TTTCAAATAT TTGTTAAGA GTTTTGATT CTTTACAATT	720
AACCGACAAA CTTCTGATA AAATATGTAC AACTTCTGAG ACTGAATAAC CTATCTCCTC	780
TTTAGAATTAA TATAATCTG TAGCTCCACC ATAATCCAA AAATACTGAT TTGTGAACC	840
TACAATATCC TCATTTCTA CGGAACCTCC TTGTATCGAA CAAATTTAT TTATCTTAC	900
CATAATACTT CAACCCCTTT AGTGTCAAAA GTAAACCAAT TCCTGTCACT GTTAAGAATA	960
GTTCCATAAT CTTATTCGAA CCAGTCTTG GTAAATTGTT TTTKACATCT ACTATYTCCTT	1020
TAGATTTATT AATATGATT TCAGTTCTC TGCCATCTCC AACTATTTA TAGTTACTT	1080
CTTCTGTCTT ATTATCTGT TTATTGTCGA TCTTGTCTT CATTGTCATA TTATCTTAC	1140
TTGAGTTAAA CTCTCCGTTCTC TTCTGGTTAC TATCAATTAC ATTATTTGAA TTAGATTGTT	1200
TTTCCCTTTT GTTTTTCTC TTTTCGTTTT TATCACTTAA ATTATTTGTT ACAATTTGTT	1260
AAAGCCCATT CTCCGTTACA ATATTGAAAT TACCATCGCT ATCACGTATA ACAGGTTCTT	1320
TCCCATTGTC ATTAGATTTG ATGAATGATA TATACCTTACCG GGATAAAATTA TAAAATTGGT	1380
TATTTAAAC GGTTATTTA CCCTTGAAT CCTCAATAAC AATTCTTCT TTACCC	1436

(2) INFORMATION FOR SEQ ID NO: 328:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 646 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

CCGGCAGACA GGAGAAGGTG TTAAATATCA ATCTCAAATG GTTCGTCAAT GGTTCTGAT	60
ACGTATTTTC CGTCTTCTT CCGTTGCTTG ACACACTCTG TGAGGAGATA TTGATTTGC	120
CCATTGACTG AACGAAAGTC GTCTCTGCC CATGATGCGA GTGCAGCGTA TAACTTTGTT	180

1353

GAGAGTCGAA	GGGGGATCTG	CTTTTTTTA	GCTTCAGCCA	TCTTTAGTAA	AGGCTTCCTG	240
TGTTGACAAT	TGGTTGTGCA	TCATGATTGC	CACAAAGAAC	GACAAGGAGA	TTTGAAACCA	300
TGGCAGCTTT	TCGTTCTCG	TCAGTTCTA	CCAATTCCCC	TTCATTGAGC	CGTTCTAGTG	360
CCATTTCAAC	CATTCCTACA	GCACCATCTA	CAATCATCTT	CCGTGCATCA	ATAATGGCAG	420
ATGCTTGTG	GCGTTGAAGC	ATAACGGCAG	CAATTCTGG	AGCATAAGCT	AGGTAAGTGA	480
TACGTGCTTC	AAGGATTCC	AAGCCAGCAT	CCTCAACACG	ACTTTGGATT	TCTTCACGAA	540
TACGGGTAGC	AACAATTCTG	CTAGAGCCAC	GGAGACTACC	TTCATCTGCG	TGCCCATCAC	600
CCGGAGTATC	CACATTAGGA	GACACATCGT	AAGGATAGAT	GGGGAC		646

(2) INFORMATION FOR SEQ ID NO: 329:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1653 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

GTTCAGGTG	CAGTAGGTGT	TACTTCAGAT	ACATTTGAAC	GTGCAGAGGC	TCTTTTGAG	60
GCAGGAGCGG	ATGCCATTGT	TATTGATACT	GCACATGGTC	ATTCTGCAGG	TGTCCTTGCGT	120
AAAATTGCCG	AGATTCTGTG	TCATTCCCA	GATCGGACTT	TGATTGCTGG	AAATATTGCT	180
ACTGCTGAAG	GTGCACGTG	CCTTTATGAA	GGGGGTGTAG	ACGTTGTTAA	GGTTGGTATT	240
GGACCAAGGTT	CTATCTGTAC	TACTCGTGTG	ATTGCTGGTG	TTGGTGTCC	GCAAGTAACA	300
GCTATCTACG	ATGCTGCAGC	TGTTGCGCG	GAATATGGTA	AAACGATTAT	TGCTGACGGT	360
GGGATCAAGT	ATTCTGGAGA	TATTGTAAGA	GCACCTGCTG	CAGGTGGAAA	TGCTGTTATG	420
CTTGGATCTA	TGTTGCTGG	AACTGATGAA	GCTCCAGGCG	AAACTGAAAT	CTTCCAAGGA	480
CGTAAATTCA	AGACTTACCG	TGGTATGGGA	TCAATTGCTG	CTATGAAGAA	AGGTTCAAGC	540
GACCGTTATT	TCCAAGGTT	TGTCATGAA	GCAAACAAGC	TTGTTCCAGA	AGGAATTGAA	600
GGTCGTGTTG	CTTATAAAGG	AGCCGCAGCT	GATATTGTTT	TCCAAATGAT	TGGTGGTATT	660
CGCTCTGGTA	TGGGTTACTG	TGGTGCAGCT	AACCTTAAAG	AACTACACGA	TAATGCTCAA	720
TTTATTGAAA	TGTCTGGTGC	TGGTTGAAA	GAAAGCCATC	CTCATGATGT	GCAAATTACT	780
AATGAGGCAC	CAAATTATTC	TATGTAAGA	ACAATGAAA	GAACCTCCAGT	AAAAACAGGA	840
GTTCTTTAC	AATGTTGTCA	ATTTCCATT	ACAGCAGCTT	TACCATCCTG	AATAGTGAAG	900

1354	
ATACTTAGAT TTTCTGGCAG ATTTGAGAAGA TGGCTAAAGC TTGTTGTTGT GATAAAGGTT	960
TGGATTGATT GAGAAATCGT TTCTAATAAT TTTAACTGTC TAGTGTGTC AAGTTCACTC	1020
ATCACATCGT CAAGCAGTAA TATAGGAGAT TCTGTGGTAA TGCTTTCCAT TAATTCGATT	1080
TCTGCTAATT TTATCGAGAG GACGAGACTA CGATGTTGAC CTTGGCTTCC GAAACTAGCA	1140
TCCATCCCAT TTATATAAAA AGAAATGTCA TCTCGATGAG GACCGACACC AGTATTCTTT	1200
TTAAATAAACT CTCTGGATCT ACTTTTTCTC AAAGCAATT TGAAAGATTG GGATAAGTTT	1260
TGTTTGTCAAGT TTATATGTAC AGAAGATTGA TAGGATATTG ACAACTCTTC GATCTGATTA	1320
GAGAGTTCAA AATGTTCTT ACGCCAAAT GATTCTAGTT TTTTTATGAA ATCTAAGCGG	1380
TGATTCACTT CACGACATCC ATAATCAACT AGCTGATCAT CTAACACAGA AAGGAATGTT	1440
TCATCTATT TTTGAGCTGA TTTTAGGTAA GTGTTCTTT GCTTTAGGAT GTGGTTATAA	1500
TTGGTTAAGT CAGATAAATA GATGGCCTTA ATTGCCCCA GTTCCATATC AATGAATTTT	1560
CGTCGAATCG AAGGTGCTCC TTTAATTAGT TGTAAATCTT CAGGAGCAAA TAAGACAACA	1620
TTCATGTGTC CTACATAATC TGAAAGCGT GCC	1653

(2) INFORMATION FOR SEQ ID NO: 330:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

GAAACACTGT ATTTCAAAGC ATTTTTGTT AGTTAAAAT TACTCCCATT CTTCTTTCC	60
AAACGTACAA TATATCCAAA ACCATTCAAAT ATACTAGATT CTATTTTTA TAATATCACT	120
AAATCCACCT AATTATAGGA CGTTTCAGA TTTTAGTCC CAGTCCCAGT ACCGGAGAAA	180
TATTGTTTTA ATATAATATC TCTTTTTGTC TTCTAAGCTC TTAAAAGCAA AAGAACAACT	240
AAAGACTCAA GACAAGGATA AAAAGCCAT ATTAGGGCAA ATAAAAGCT TTAAGACAGA	300
TGACAAATCT AAGTCAAATA AGAAAGACCA TAGCAAAGGT GCAGAGAGAT AAATATTGGC	360
GGTCTTCGGA CTGCCTTTAT TTTTTATCC ATTTCCTAAA TCAAATTATC TCAGACTATA	420
TATGCACATA TACACTAAA TTCAATATAAA AACATGGCTT GTAAAAAATT ACTTTAATCA	480
CAATAATCGC ATTTAAAATT GTGATGTTG CAAGCTAAAT TACGGACTTC ACTTGGAAAGT	540
TTTCCCTGT ATCTTTATAA ATAGATAGAA AATTGCTGG CAGATGAATA TCCAACAGAT	600
TCTGCTATCT CTTTTATAGG TAGTTCACTG TTTAAAAGAA GAGTTTCAGC TACATTCAATT	660

1355

CTTTTTCTTT GAGTGTACTC TGTAATGCTT TGACAATATT TTTCCCTTAAA TAAATTTTTT	720
AATTTAGTAC CACTCATTTT AGATATTTTT TCAAGCGTGC CTTGATTTAC ATTCGTTGCA	780
AAATGATCAT CTAAGAATCT TGCTACATCT TCAAGTGCTT TATCATCATC AATTTCAATT	840
TTATATTTTT TTCTATTTAA GTATGTGTCA ATTACTATAC TTATCCATTC ATTTGCCTTT	900
GCTTTAAAGA AAAAATCAGC GGCAGGAGCG TCCATCTTAC AATTTAATAT TTCCATTGCC	960
ACTCTTTCTA AGGCCTTTGT AAGTATTATT TGATTCGGTT GAAGCAAGGT TGAATAAAA	1020
GATTCTGGAT TAATGTTAAT AGATGCTAAA TGTTTTCTA TTAGCTCTTT TTTAAAACm	1080
ATGGAAACAG CAAGATAACA ACAATTCTCG TGTAATAAAA AAACAAAATT ATCTTTTATA	1140
TTATCAAAT CAAAAGTACA TAGAGAGTTT GCGGTAATAG TTTGATACGG ATTAAACTTT	1200
TCTCCGTTTG CACTGACAAT GTAACTTGAA TAAATTGAAA CATACTCTGA CATACTATAAA	1260
GTGCTATTTT GAACACTTC CTCTTGATA TAAAATCAT GTATATCGAT AATGAAGATG	1320
CCTCCTTCAT AAAACCGGA	1340

(2) INFORMATION FOR SEQ ID NO: 331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 607 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

TATGTTCTGT ATGAGTTTTT AAGTAGGAAA AACGTGCTAA CCTCTCAGAT TTTGGAACCTT	60
GTAAAAGAAA CTCTTTTTTC ACCCGTAGTA GTTGATAATG GGTTTGATCC GGCTTATTT	120
GAAATTGAGA AAAAACAAATT GCTAGCAAGT TTAGCAGCTG ATATGGATGA TTCTTTTAT	180
TTTGACACATA AAGAATTGGA TAAATTGTTT TTTCATGATG AACGTCTTCA ATTGGAATAT	240
ATGATTTAC GAAATCGTAT TTTCAGCTGAA ACTCCACAAA GTTCTTATTC TTGTTTCCAA	300
GAATTTTTAG CCAATGATCG AATAGATTTT TTTCCTCTAG GTGATTTAA TGAGGTTGAA	360
ATTCAAAATG TATTAGAAC TTTGGCTTT AAAGGTCGAA AAGGAGATGT GAAGGTTTCAG	420
TATTGTCAAC CTTATTCTAA TATCCTTCAG GAAGGTATGG TTCGGAAAAA TGTGGGACAA	480
TCCATTGGG AATTAGGTTA TCATTACTGT TCTAAATATG GTGATGAGCA ACATTTACCC	540
ATGGATTGAA TGAATGGTTT ACTTGGTGGAA TTTGCTCACT CTAAGCTCTT TACAAATGTC	600
CGGGAAA	607

1356

(2) INFORMATION FOR SEQ ID NO: 332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 900 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

TTAAAATACC	GAATTGGT	TTGCTCTA	TTCAACATT	GTGAATGCC	TCAGGCAGAG	60
AACCGATACT	AAAGATAAA	CCAAAATAGT	TGTCATTCG	TTTACCGATA	TCAATCTTAT	120
TGGTTAAATC	AAAATCCAGT	TCGTCAATTG	CGCCATCGAT	GTCTTGATTG	ATTTCCAAA	180
GTGTTGTAAT	GAGGTTACCC	GTACCGCCTG	GGATAATCCC	TAACCTAGGA	ATGTAGTCTC	240
TCTCATCAAT	ACCTGAAATG	ACTTCATTGA	CAGTTCCATC	TCCACCAAAAC	ACAACCACTG	300
CATCATACTG	CTCACGAGAA	GCTTCTTCAG	CAAATGTGT	TGCATCCAGC	GCTTTTCGG	360
TAATTTGGT	TTCAACATAT	TCAAAGTATT	CTTTGCTTT	ATTCTCCAGC	TTTTCTTTGT	420
AATCCAAAGC	CTTCTCGCCA	CCAGAAAGTAG	GGTTGATAAT	TACCATGGCT	TTTTTCATTG	480
ATTTTATCCT	TAATTTAAA	CAGAAATGTT	TACATTTCGT	CGTATGCAAG	TAAATGTAAT	540
CCTATTATAC	AATGAAAATA	CAGAAAAGAG	AAATCTGACG	TACTGGAGAT	TAATACGCTT	600
TTATTCTATT	TTCCCATCGC	CTAACTACAT	CCTTTAAGGG	TTCATCCAAG	TAAGAATAGG	660
CCTTATCCTT	GATCCAATCA	GGAAATACCGT	AAGCTGCCTC	TGCTAwGCTA	CAAGTGATTG	720
CTGGAGAGT	ATCACTGTCG	CCACCAAGTG	AGATGGCATT	TCTTATCGCA	TCTTCGAAGT	780
CTCTACTTTC	AAGAAAGGCG	ATAATGGCTT	GAGGGACAGT	TCCCTGACAT	GTTTCGTTAA	840
AACGATAGTT	AGGACGGATT	TCATCTAAAG	TTTGAGATAG	ATTGTAATCG	TATTCTTTT	900

(2) INFORMATION FOR SEQ ID NO: 333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

CCTTTCTGGC	ACACTGGTCT	TGGAATACGG	AAAACCTCT	AAAATATCT	ATGCTGGAAT	60
GGACGAGGAA	TACCGTCGTT	ATCAGCCTGC	CATCATCACT	TGGTACGAAA	CAGCCAAACA	120
TGCTTTGAT	CGCGGACAGA	TTGGCAAAAT	ATGGCTGGAA	TCGAAAACGA	CCTCAAGGGC	180

1357

GGTCTCTACA GCTTTAAATC CAAGTTCAAT CCGACCATTG AGGAATTCGC TGGTGAGTTC	240
AACCTGCCAA CTAATCCTCT TTACCACCTC TCCAATCTGG CCTACACTCT CAGAAAGAAA	300
CTGCGAGaA GcATTAACAG AAAGGAAGCC TATGACCTTT AAACCTCTCA GCCAAGAAGA	360
ATTCATCCAG CATAACCTAG CTAGATCCC ACGCTTTT ATGCAGACCG TAGAAATGGC	420
AGAGCTGCTG AGCAAGCGTG GCTTCAGTAC CCAGTATGTC GGCTACACTG ACCCACAAGG	480
GAAGGTAGTG GTGTCAGCTG TCCTCTACAG CATGCCTATG ACTGGTGGCC TTC	533

(2) INFORMATION FOR SEQ ID NO: 334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 544 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

CCAGCAAAC AGGAAGCTAG CCGTAGTTGC TCAAAGCACA GCTTGAGGT TGTAGATAAG	60
ACTGACGAAG TCATGTACAA AACACTGTT TGAGGTTGCA GATAGAACTG ACGAAGTCAC	120
TCAAAACACT GTTTGAGGT TGCAGATAGA ACTGACGAAG TCACTCAAA CACTGTTTG	180
AGGTTGCAGA TAGAACTGAC GAAGTCAnA ACCACACCTA CCCCCAACTG AATCTGAAGT	240
GGTTTGAAGA GAGTACAAC TGTCTTTAG AAAAGGAGCC TATAATGAAA GTCTTTCAGC	300
ATGTAAATAT CGTGACTTGT GATCAAGATT TCCATGTTA TCTTGATGGA ATCTTAGCAG	360
TCAAGGATTC TCAAATCGTC TATGTCGGTC AAGATAAGCC AGCGTTTTA GAGCAAGCTG	420
AGCAGATTAT AGACTATCAG GGAGCTTGGA TTATGCCTGG TTTGGTCAAT TGTCACACCC	480
ATTCTGCAAT GACAGGTCTG AGAGGGATCC GAGATGACAG CAATCTCCAT GAATGGCTCA	540
ATGA	544

(2) INFORMATION FOR SEQ ID NO: 335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

CCAGGAACTC AAATGTAAGT AGGGGTTCCCT TTTTTGTATA TTTTTCAAAT AACGCCTCTA	60
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CACTATTTGT AGCAAATTCA CCAACTACAG TTGTATCTTA GTTAAAATAA GTTAGAATAT	1358 120
GTAAGTGAGT ACCAGATATA CCAAGACATC GTCACCATCT AAGGTATATT CAAAATACAA	180
AAGTTGACCA ACTAGATTTC TGAATATCCT TATATATCCA TTCTTAAAT TGGTTAAAT	240
AGCGTAGTCT TTTAAACTAG TTTTGAGAAT CCAAAAATC TTCCCTACATA TGTAAGAAGA	300
TTTTTTAGTT CAGAATGATT AGaTTTAGCT AATGGATACC TATCCTACC	349

(2) INFORMATION FOR SEQ ID NO: 336:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1206 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

CTCCGATAAC CACACCAGCA ATGAAATAA TTCCATCGTT AGCATCAAGA ACACCCGCAC	60
GCAGGATATT TAAACGACCT GCAAAATTG AATCAATTTC GTGATTGTT TCTGACGCTA	120
AATTTCAAGT TCAAGTTAGC CATCAAGAAG TCTTCTCTGG GTGACTTGTA GTCCAAGCAT	180
TTTTTAGGAT AGTTGTTAAT CCACTTTCG ATGAATGCGA CTTCTTGGG AGTCATTTTC	240
TTGGTTCCCT TAGGTAAACCA TCTACGAATG AGCCTGTTGT GATTCTCATT AGTTCCCGGG	300
ATCCCTCTAGA GTCGACCTGC AGGCATGCAA GCTTGGCACT GGCGTCGTT TTACAACGTC	360
GATGACTGGG GAAAACCTG GCGTTACCCA ACTTAATCGC CTTGCAGCAC ATCCCCCTTT	420
CGCCAGCTGG CGTAATAGCG AAGAGGCCCG CACCGATCGC CCTTCCCAAC AGTTGCCAG	480
CCTGAATGGC GAATGGGGCC TGATGCGGTA TTTTCTCCTT ACGCATCTGT GCGGTATTT	540
ACACCGCATA TGGTGCACTC TCAGTACAAT CTGCTCTGAT GCCGCATAGT TAAGCCAGCC	600
CCGACACCCG CCAACACCCG CTGACCGGCC CTGACGGGCT TGTCTGCTCC CGGCATCCGC	660
TTACAGACAA GCTGTGACCG TCTCCGGGAG CTGCATGTGT CAGAAGTTT CACCGTCATC	720
ACCGAAACGC GCGAAACGAA AGGGCCTCGT GATACGCCA TTTTTATAGG TTAATGTCAT	780
GATAAGGATG GTTTCTTAGA CGTCAAGTGG CACTTATCGG GGAAATGTGC GCCGAGACCC	840
TATTTGTTA TTTGCTAAA TACATTCAA TATGTATCCG CTCGTGAGAA AATAAACCTG	900
ATAAATGCGT CAATAATATT GAAAATGAA GAGTATGAGT ATTCTACATT TCCGTGTCGC	960
CCTTATAACCC TTTTTGCGG CATGTTGCCT TCCTGTTTT GCTCACCCAG AAAACGCTGG	1020
TGAAAGTTA AGATGCTGAA AAATCATTG GGTGCACAAAC TGGGGTTACA TCCAACGGAA	1080
ATCTCCAnCA GCAGTTAAGA TCCTCTGACA GTTGTACACG CCGCAAGAAC TATTCCCGAT	1140

1359

GAATGAGCAA CTTTTAAAAG TCCTGCGAAT GTTGGGGCGG TAATAATCCC CGTGTGTAG	1200
GCCCCG	1206

(2) INFORMATION FOR SEQ ID NO: 337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

CTGCTCAACT CAGACAGTCA AATTCTGAC TTTACCAAAA GAACCATCAA AAAAGTTGCT	60
GAAAAAGGCC ATCAGGTTAT TATTACGACA GGTCGCCCTT ACCGTATGTC AAAAGATTT	120
TACCGTGAAC TGGGCTTAGA CACTCTATG ATTAACCTCA ACGGATCCCT TACTCATTAA	180
CCAGACCAAG TTTGGGATTT TGAAAAGTGT TTGACTGTAG ACAAAAAATA TCTGCTAGAT	240
ATGGTTCAAC GTTCAGAGGA CATTCAAGCC GATTTTATCG CTGGAGAATA TCGTAAAAAA	300
TTCTACATTA CAAATCCCAA TGAAGAAATT GCCAATCCCA AACTATTTGG TGTAGAAGCT	360
TTCCAGCCTG AAGATCAATT CCAGCCTGAA TTGGTGACCA AGGACCCCTAA CTGTATCCTC	420
TTCCAGACTA GAGCCAGTGA CAAATATTCC TTGGCAAAAG AAATGAACGC CTTCTACCAAG	480
CATCAACTTT CTATCAATAC CTGGGGAGGT CCGCTCAATA TCCTTGAATG TACCCAAAAA	540
GGTGTCAACA AGGCCTTGC TTTGGACTAC TTGCTCAAGA TAATGAATCG TGACAAAAAA	600
GATTGATTG CCTTTGGAGA TGAACACAAT GATACCGAAA TGCTCGCTTT TGCTGGGAAG	660
GGTTATGCCA TGAAAAATGC CAATCCAGAG CTACTCCCTT ATGCAGATGA GCAAATTCC	720
CTTACCAACG ACCAAGATGG GGTTGCCAAA ACCCTACAAG ACTTATTCTT ATAACCTATA	780
CTGATACTCA ATGAGGGGCA AAGAGCGAAC TTA	813

(2) INFORMATION FOR SEQ ID NO: 338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 683 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

CCTAGATAAA TGATATAATT CTATTATTGT TCGTAAAAT TAAAAGGAGA TTGATGATGG	60
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1360	
ACAAATTATT TAAACTAAAA GAGAACGGTA CAGACGTTCG TACAGAGGTT CTCGCTGGTT	120
TAACAACTTT CTTTGAATG AGCTATATTG TCTTTGTAAA CCCACAAATA CTTTCACAAA	180
CAGGAATGCC TGCTCAGGGC GTCTCCTAG CGACGATTAT TGGTGCAGTA GCGGGTACCT	240
TGATGATGGC TTTTTATGCT AACTTACCTT ATGCCAAGC GCCAGGTATG GGACTCAATG	300
CCTTCTTAC CTTTACAGTT GTATTCGGGC TTGGTTATTC TTGGCAAGAA GCCCTAGCTA	360
TGGTCTTCAT CTGTGGGATT ATTTCAATTGA TTATTACCTT GACAAATGTT CGTAAAATGA	420
TCATTGAATC GATTCCAAT GCTCTTCGCT CAGCTATTTC AGCTGGTATC GGTGTCTTCC	480
TTGCCTATGT AGGGATTAAG AATGCTGGAC TTTGAAATT CACGATTGAT CCAGGCAACT	540
ATACTGTTGT AGGAGAAGGG GCTGACAAAG CTCAGCAAC GATTGCAGCA AACTCTTCAG	600
CAGTTCCAGG ATTGGTCAGC TTTAATAATC CAGCTGTTT AGTGGCTCTT GCAGGACTTG	660
CCATTACTAT CTTCTTGTC ATC	683

(2) INFORMATION FOR SEQ ID NO: 339:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 852 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

CTACTTTACA TGGAAAGTAGT CACTGAATTC CAGTTAGAAA TTACTTTGTA ACTACGTTTT	60
GAGGAGGAGT AAAATGCTTT CCTACGTTCG ATATTACCCA CTAGCGATAG CTAAATTAAT	120
GTGTCTGTGC TCTCCAAAAA TCTGCTGATT TATTACTGAC TAATACAGGA GGTTTTTTTT	180
ATGgACAGAC AATCATATCT GCTATTGGTG TTTATATTTC CACCACTATC GATTATTTAA	240
TTATTTTAAT TATTTTATTT GCACAGCTAT CACAGAAATAA ACAGAAATGG CATATTTATG	300
CGGGGCAATA TCTAGGCACA GGCTTACTTG TAGGGCGAG TTTAGTTGCT GCTTATGTCG	360
TTAATTTCGT GCCTGAAGAA TGGATGGTTG GATTGCTTGG TTTAATCCCT ATCTATTTAG	420
GGATTGCGTT TGCAATTGTT GGAGAAGATG CGGAAGAAGA AGAGGAAGAA ATTATTGAAA	480
GATTAGAACAA AAGCAAGGCA AATCAACTGT TTTGGACAGT TACATTGCTG ACAATTGCGT	540
CTGGCGGAGA TAATTAGGT ATCTATATAC CTTATTTGC TTCGTTAGAT TGGTCACAGA	600
CCCTCGTGGC CTTGCTTGTG TTTGTAATCG GCATAATTAT CTTTGCGAG ATTAGTCGGG	660
TGTTATCCTC TATTCCGTTA ATATTCGAGA CAATTGAAAA ATACGAGCGA ATCATTGTC	720
CCTTAGTATT CATTCTACTT GGACTATACA TCATGTATGA AAATGGCACG ATAGAGACTT	780

1361

TTCTGATCGT GTAGATTTTT TTGTTTCACT AGGGATTTAG CCCGAGCTCA AATCAGCTCT 840

CTGATTTTCA GA 852

(2) INFORMATION FOR SEQ ID NO: 340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 754 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

CCGCACAAAA CGGCATAGTA TCAAGATTCT ATAAAGCCTT GATACTATGC CTTTTTAATG 60

GATAAAATAGT TAGTCTTTTT TAAAGACCGG ATCTTTCAAA CTCTGCATAC TGGCATTGAT 120

CACCGCGCCT AGGATAACAA TTTTAGCAAT CAAGATAAAC CAAAACATCA TAACAACAAG 180

AAGAACGGAA CCTAAAATTC GGACATCCAC CAAATGATGG ACATAGTAAT TGAGATAACT 240

AGAGAACAGA GTTAGTAAAC CTAAAATCAC TAAGAGAACAA AAGGCACTGC CTGGTAGGGT 300

ATAGCTAATT TTCCTGTTAG ATAGATTGGG AAGAAAATAA TAAAGCATGA CCAAGATAGC 360

AAAGAGGAGG GCGTAAATCA GAGGACCTGC CAACCCTGT AAAGCCTGAT AGATAATGCC 420

ATCTTTGTC CAAATAATGAG CAAGTAAAGC CAAAATCATC TGACCAAAATA AGATCAAAA 480

CAAGGCAAC GCAAAGAGGA GCTGCAACCA AAACTGACTA GGAGACTTAG CATCTGATGG 540

GAAATAAGTC CACGACTCTT TTCGACGCC TAAGCCTGT TAAAAGCTTT TTGCAAGAAA 600

TTCATAGATT TTGAAAATCT CCATAACGCC GATAAAACAG AAAAACTCAA TAAACCTGTT 660

GAAGGTTGCG TCAAGACTTC TCTGGCTATT TTTTCCACAC CTTCATAGAG GCTTGGGGGG 720

CAGACGTCTT TCATAAAAGCC CAAAATTCT CCCA 754

(2) INFORMATION FOR SEQ ID NO: 341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 707 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

GGGGATAACT CTAGGAGTAC CGCTATTACT CGACTTAATG AGTGCACAAG AAGTCAGGAT 60

TTTTATGCAG GTTGGCGCT TCATCAGACA GGGAAAGATTT ACAGCGACTA TTATGGAAGT 120

CAAGGTTGC TTTATTATTT GCTGACTTAC GTGAGTCAGG GCGGATTTTT CTTTGCCATC	1362 180
TTTGAGTGGT TAGCCTTGGT AGCAGGAGGA TTTTCCTTT TTAGATCAGC GGACACCTTG	240
ACAGAGCAAG GAGACCAAGC TGGACATCTG GTGACTATTT TTTACATGCT AGTTACAGGT	300
CTTGCTTTG GTGGAGGCTA TGCGACTCTT TTAGCGCTTC CTTTCTTATT CGCAGCCTTT	360
AGTTTAGTTG CGGCTTACCT AAGCAATCCA ACCCATGATA AGGGATTTGT ACGGATTGGG	420
CTAGCTTGG CAGGCGGATT TTTCTTGCT CCTTATCAT CGCTCCTGTT TATTGCTGTA	480
GTGAGTTAG GCTTGTGGT CTTTAACCTT GGGCATAGAC GCTTGCACCA TGGGTTTTAT	540
CAGTTCTTG CAGTGGCTTT AGGTTTTCA CTTGTCTTT ATCCAATGC CTACTATAGT	600
GCTGCAACAG GAAGTTTGG GGATGCGwTT AGTGGTATTC GTTATCCTAT TGACAGTATT	660
CGCTTGATT TTACTTCTAA AATTTAGAG AATATGTTT TTTAAGG	707

(2) INFORMATION FOR SEQ ID NO: 342:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 762 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

GGATTTGAA AAACCATACC GATTGACGA CGTATATTCC AAACATTTTC CTCAGTCAAA	60
CGTTGCCAT CAATTACAAT CTCCTCCGGAT TCTGCTTCCA GTAAGCCATC AATTAATCGA	120
ACCGTCGTG ATTACCACT ACCATTATGC CCTACAATCG AAAGCCATTC TCCACGTTTC	180
ACGTGAAgT AATATCCTTC ACATCGTAGT AGTTCTGATT TTCTTTATAG CGAAAAGAAA	240
GATTTTTAC ATCAATTATT GATTCATTT CGAACCAAAT GTCCCTTAA ATACATAGGC	300
ACTACCTTG AAATAGTCAT AGCCAGAGTA GATACTGAAA AATAAGGCTA CATAAAGTAG	360
AACTTGACCA AGCAAAGTCC AATGTAATAG CAAGAAAATA ATGGCAAACA TCTGACTAAA	420
AGTTTAATT TTTCCAGGCA TTGCTGCTGC TAAAATTGTT CCACCAAGTTT CAACCAATAA	480
AAGCCTTAA CCTGTACAG CTAACCTACG ACAGATAATC ACTGCAACAA TCCAAGCCGG	540
AGCCATACCT AACTCAATCA ACATAATAAA AGCCGACATA ACTAGTAAC TATCCGCCAT	600
AGGATCTGCA AATTACCAA AATTACTGAC CACATTCCAT TTACGAGCTA AATATCCATC	660
TAAATAGTCG GTAATACTGG CAACAGCAA GATAATAGCT GCAACTATAT GACTCTCTAT	720
CGAATTTCCT ATCGTTAAA TAAAGATAAA AATAGGTATA AA	762

(2) INFORMATION FOR SEQ ID NO: 343:

1363

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

CTTTTGATAC ACTTAAACTA TGAATACAAA TCTCAAGCCC AAACCTCAGC GTTTGCTTC	60
TGGCAGTGCC TTTGCCTGTC CTATCTGTCA AGAAAATCTG ACTCTGTTAG AGACTAATTT	120
CAAGTGCTGC AACCGTCATT CTTTGACTT GGCGAAATTG GGCTATGTCA ATCTAGTCCC	180
TCAAATCAAG CAATCTGCTA ACTACGACAA GGAAAATTTT CAAAACCGTC AACAAATCCT	240
AGAAGCCGGC TTTTACCAAG CTATCTTAGA TGCTGTATCT GACTTGCTTG CAAGCTCAAA	300
AACTACCACA ACAATTGGG ATATCGGTTG TGGTGAAGGA TTCTATTCTC GCAAACCTACA	360
AGAAAGTCAC TCTGAAAAAA CTTTCTATGC CTTTGACATC TCCAAAGATT CAGTCCAAAT	420
CGCGGCTAAA AGTGAACCCA ACTGGGCAGT CAATTGGTTC GTTGGCAGT TGGCACCGACT	480
TC	482

(2) INFORMATION FOR SEQ ID NO: 344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 520 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

TTTATTTTTA TAAAGTCAAT ACCTGTCTTT ACTTTTTCTT AAAAAAAAGTT TATTATGTTC	60
TTTAAGGAGG TGTAAAACAT GAAAATAAAT AATAAACTCG TTGGAGAACG TATTCAAAAT	120
ATCCGTTAA GCCATGGCGA CTCTATGGAA AAATTTGGAG AAAAATTTAA TACTAGCAAA	180
GGTACAGTTA ACAACTGGGA AAAAGGTCGC AATTTACCAA ATAAAGAAAA CCTACTAAAA	240
ATTGCATCTA TTGGAAAAAT GAGTGTGAA GAGTTACTCT ACGGCGATTA CAATACTTAT	300
CTACACTTAA AGATTATGGA TTTAGCTCCT GAATGTATAA AAAATTATGA TGAGTATAAC	360
TCTTTACACG ATGATATAAC AAATAAAGCG TTACAGATCG CTCAAAATAC CATTCTAAG	420
ATTGATTATC AAATTCAGA CGAAACGATC AAAAATTTA TTGATTTAGC TATCGAACAA	480
TCGAGAGATT TGCAAGGAAA TTTGTTGAAA AAAAACGGGT	520

1364

(2) INFORMATION FOR SEQ ID NO: 345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1003 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

GCATCAAATC CGCCATCAAA	GAAGTTCTCT GGATTTACCA	AGACCAGTCA	AATAGCTTAG	60
AAGTGCTTAA TGACAAGTAC	AATGTTCACT ACTGGAATGA	CTGGGAAGTT	GGAGACACGG	120
GAACCATTGG TGAGCGCTAT	GGTGCCGTTG TTAAGAAACA	CGACATTATC	AATAAGCTTC	180
TCAAACAGTT GGAAACCAAT	CCTTGGAACCC	GCCGCAATAT	TATTCGCTC	240
AAGCTTCTGA AGAAACAGAT	GGGCTGCTCC	CGTGCCTT	TCAGACCATG	300
GGCGTGTGAA	TGGGAAATC TATCTGGATG	CGACCTTGAC	CCAGCGCTCC	360
TGGTGGCCCA CCACATCAAC	GCTATGCAGT	ATGTGGCTTT	GCAGATGATG	420
ATTTTGCTG GAAGGTTGGG	AAGTTCTTCT	ACCTCATCAA	AAACCTCCAT	480
ATCAATTGAA ACAAGCTAG	GAATTGCTCC	GTCGGGAgCC	GTCAAACTGC	540
TGGTTTAA TGTTCTGAT	GGGACTAATT	TCTTGTAT	CAAAGCAGAA	600
TGGTGGATTA TGACCTGTT	AAGGCCAGT	TGAAGTTGA	CCTAGCTATT	660
GAAAAAAAGAA GTTGAGAATA	ATCCCAACTT	CTTTGTTTC	TTAACGTGAT	720
GAGCTGCTTT TTTACGGTTT	TCTTCGATGA	AAGCTGCTTT	TTGCTCTTCT	780
CTTTCTTTT AAATGCGTAT	ACTGCACCTG	CAACGGCAGC	GACAGTTCCCT	840
TTACAAGACC TTTAGCGAAT	CCTTTAGCCA	TGAGTCTTCC	TCCTTTATAT	900
CCAGCCTCCT	CAAGAGGTCA	CATTTCCTG	ACTGACCTTT	960
CGAAAAAAATG GGAATTTC	AAGGAAAAAA	GATGAGAACAA	AAA	1003

(2) INFORMATION FOR SEQ ID NO: 346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

CCGCACGTAC TATTCCAGAT	GCCGAGGAAG	TGGACCTCAT	CCTCGTTGGC	GCAACTGGTC	60
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1365

TCAACGCCCT	TGAACGCCCT	TTGGTCGGCT	CTTCATCTGA	ATACATACTC	CGCCATGCTA	120
AGGTCGATTT	GCTGGTTGTG	AGAGAACAAAG	AAAAAACCTT	ATAATCACAA	AGAAAAGGAG	180
CCCCTAGCTC	CTTTTGTGTT	ACGATTTATT	TCTCTCTTAA	TGGCGTTCGT	AAGCCTTGAG	240
CTGGCGCTGC	AGTTCCCTTT	TAATAGCAGG	TTCTGGAGCA	TATTTTCTT	CCCAATTATC	300
TGGTTTTAAG	ATTTTATGGG	TCACTGGATC	AAAATGAGCC	TTGCCATCTG	GAAAAATT	360
CCCCATATTG	GCCTGATGGA	CAATATCAA	AATACGTTCT	GGGTCCACCC	CCATCAAGAC	420
AAAACTGCCG	TAGGTGAAGT	AAAGCGTGTC	AATCAAGGCA	TCCACTGCC	CTATCAAATC	480
TTGCTGAGCA	GGTGTCTTCT	TGGCTACTTT	ATCTGCTGCC	TTATCAAGGG	CCTGATGAAG	540
TTGCGATACA	GCTTGACCAA	AATCTTCTTC	AGAAGGACTG	GCTGCTCGA	CAAACCTCCAC	600
CAATTCTTCT	ATTTTAAAC	CAGCCCTATG	GGTTGCACCC	TCTAAATCCC	AAGCTCGAGG	660
TTCTTCTTGG	GTTCGTTCAT	CCATCATGTG	GTGAAAGTC	TTGACCTTAT	TGAAATGATA	720
GTCACGGCTG	ACAAAGACTT	TTTCTGAAGA				750

(2) INFORMATION FOR SEQ ID NO: 347:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 596 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

CGCAACATAC	GGATAACCTC	CAAAGAATAT	TTTTATATTA	TAGCAAAGCT	TTAAATTGAA	60
TGTTAGAGTC	TTGTTCAAAA	CAATCATCAA	AACCACGTGG	ATGATGGTAT	TCTACTAACT	120
GTTGATCTTG	AGGATAAGTG	TACTTACCGC	CAACTCCCA	GATAATGGA	TGGAAATCGT	180
ATTGCAAGCG	ATCTTTTCGC	ATTTTCCAAA	GTTCTAGAAT	CTCATTAGTA	GAAGCCATGA	240
AGTTAGACCA	GATATCATAG	TGAACGGGA	TAATGACTTT	GGTACGCAGA	TTTTCTGCCA	300
TACGAAGAAG	GTCGATAGAT	GTCATTTGT	CTTGGATAACC	TACCGGATTT	TCACCATAGT	360
TATTCAAAGC	AACATCAATT	TTAAAGTCTT	TACCATGTTT	TGCAAAATAG	TTTGAGAAGT	420
GAGAATCTGC	ACCATGATAG	ATGGTTCCAC	CTGGTGTTC	AAAGATATAG	TTAACAGCCT	480
TTTGAGCCAT	TTCTTCATCT	GTAACAGCCA	AGCCAGCAGT	TCACCGCCTG	TCTCATCAGC	540
ACCGTTCACT	GGGAGAGTTA	CCAAGCAAGT	ACGGTCAAAT	GATTCTACTG	CATGAA	596

(2) INFORMATION FOR SEQ ID NO: 348:

1366

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 673 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

CAGAGTCAAC AGCCTGAGTT GAAGGCAACT TTAGACACAG CAGTTACGAC AGCTGAATGA	60
GCTCCTCCAT CAGTTTTTC TTTAATGAGT CCAGCTACAT CTTCAACTTC GAGGCCGTTA	120
ATCACAATGT CAGCGCCTAC TTCTTTGCA AGGGCAAGTT TGTCATTGTT GATATCGACT	180
GCGATAACAT GAGCATTGAA TACTTTTTA GCGTATTGAA CAGCGAGGTT ACCAAGTCCA	240
CCAGCACCGT AAAGAACAAAC CCATTGGCCT GGTTCAACTT TTGCTTCTTT GATAGCTTTA	300
TAGGTTGTTA CTCCAGCACA TGTGATAGAA GAAGCTTGGG CTGGATCAAG TCCGTCAGGA	360
ACTTTGACAG CATAGTCAGC AGTTACGATA CATTGTTCAAG CCATACCAAC GTCTACTGAG	420
TAGCCAGCAT TTTTCACTGT ACGGCAAAGG GTTTCGCGAC CAGTTGTACA GTATTGCAA	480
GTGCCACATC CTTCAAAGAA CCAAGCAACG CTGACGCGGT CACCGACTTT AAGGCTTTTC	540
ACATCTGGAG CAATCTCTTT AACGATAACCG ATACCTTCGT GCCCAAGAAC ACGTCCTGGG	600
ACTTGACCAA AGTCACCATG AGCAACGTGG AGGTCGGTGT GGCAAACGCC CACAGTATTG	660
ACTTCTACAA GTG	673

(2) INFORMATION FOR SEQ ID NO: 349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

GTACCCCTACA AATGCTTTAC AGTATGGTT GAGGGTGGTC AATGGAACTA TGGAGTAGGT	60
TGGACAGGAA CTTTTGGATA TTCTGATTAC TTACATTCTA CTCGATATCA TACAGCAACT	120
GTTAGACATG GGGGTAGAAC CTCTAAGGGAT TATGCAAAAC CTGAGGCATG GGCTAGAGCT	180
TCCCTCACCA AGATTCCG	198

(2) INFORMATION FOR SEQ ID NO: 350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid

1367

(C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

GCTTCTTCTA TAGACAAAAA TATCATGGGT AAAATAATCA AGGCTATAGC TAGAAGGAGG	60
GACCAATCCA CTACTAATCC TAAGAACAAA ACACATCAAGA GAGCAGAAGA GAGAGGTTCA	120
CTGGCACTGA TAACGGCAAC CACCAAAGGA GAAACCAAGG ACACAGCCTT CATGGAAATG	180
AAAAAAAGCAA AAGCCGTTCC AAAGAAAGCG ATAATGAGGC AAATCAAGAT ACTCCAAATA	240
TCAAGAGTAA AGGAAAGCTG ATAAACCGGC GAGAGGACAT TGCTAAACAA ACCTGCCAAA	300
ATCATCCCCC ACCCAACCGT AGGAACAAAAA CCATAACGCT TAGCAAAAGG TTGGGGCAAG	360
ATAACATTTAA ACATAACACC CATGGCACTC AGCAAACCTG TTATAAGAGC TAGGGCGTC	420
ATGGATAACT GAGAGAGGTC TCCCTTGTC GCCATCAAGC AAACACCCAG CATGGCAACC	480
AAAACATAGA AAACAGCGCT TTTTGACGCT CGTTTTGAT AAACCAAGCG ATTGTAAAAG	540
AGGATAAAAAG CAGGGCTAAT AAACGTAAA ATAGTTGCTG TCGTAGCATT TGACTATTCT	600
ACACAGAGAT AGAAAAAATA CTGAACGTAA AAAATCCCCA AAATAGCATA GGCTAAAAAG	660
GGCAGGTTAAT TTTCTTGTC TCGCCAAATA TCTAGCACTT GCAGTTTAA TTGTATTGCA	720
GACCAATGA GTACAAGACT CCCTGCCAGT GTCAAAAGCA TACACCTAAT CCAGCCCGAA	780
GACACCTGAT AATGAGTAAA GAAGTACTCT CCTAAATTC CACAGATTCC CCATATTAAG	840
CCGGATAGGA GCGAATAAT TTTCCGTTA ACAATCTTTT TCTGATACTG A	891

(2) INFORMATION FOR SEQ ID NO: 351:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

GAAAGCCGTT AATAGAACAT TGCTTTTTA TTTTTAGAGT AAGCTAAGCG CTTCAGCAGTC	60
TGCGATGATG GTTACATCAG GGTGATTTG GAGGCTACTT GCAGGTAGGT TCTCAGTCAC	120
TGGGCCAGAT ACTGTTCCGG CAATGGCTTC TGCTTCGAC TCACCGTAAG CAAAAGAAT	180
AATAGACTTG GCATCCAAA TGTTTTAAT CCCCATTGAA ATAGCTTGGG TTGGGACGTC	240
TTCAATCTTG GCAAAGAACG GTGCATTGGC TTGATAGTA GACTGGCAA GTTCTACTAG	300

1368

ATGCGTTGAGCTGCAATG GAGTG

325

(2) INFORMATION FOR SEQ ID NO: 352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

CAAGAGCACT TTGATGATTT TTGATAAGCA TCGAATTAA AAATACAAAT ATGGCAATCG	60
CAAGTTTGG TGTAGAGGCT ATTATGTAGA TACGGTAGGC CGTAATCAGA AAGTGATAGC	120
TGAATATATT CAGAATCAAT TACAAGAAGA CAGAGTAGCA GACCTAGCTC ACGTTATTG	180
AGTCAGTAGA TCCGTTTACT GCCGAAATAA ATAAGAGGAA GTAACGThAA GTGCTTTAGC	240
ACCTGCTCGG GAAAGTGGTG CGCGAGGAAG CTATTCAGG ATGCTTTGGC CCTGGCCGGT	300
AGAAGCGTTA TAGCCGCAGA CTACGACACT TCACACTGGT GGTT	344

(2) INFORMATION FOR SEQ ID NO: 353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 692 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

CCCTATCCCT GCTATTGGGG CTGCTCTCAT TGCTGCTTTG GCACAAATCA GTCTTCCAAT	60
TGGACCTGTT CCCTTCACTC TGCAAAACTT TGCAATCGGC TTGATTCTAC TGTCTTTAGA	120
CCGAGAGAGG CTGTACTTTG TGCTGGACTC TATCTTCTTC TAGGTGCTAT CGGTCTTCCT	180
GTCTTTGCAG GAGGTGGAGC TGGTTTCAG GCTTTAGTTG GCCCTACTGC AGGCTATCTT	240
TGGTTTATC TCGTTTACTC TGGACTTACT TCCTCTCTAA CCAACAGCAA GAGTGGTGTT	300
GTAAAGATTT TTCTTGCAAA CCTCTTGGGT GATGCCCTTG TCTTGTGG CGGGATTCTC	360
AGCTTGCACTT TCCTAGCTGG AATGGCATTG GAAAAAGCTC TTGCTGTGGG GGTTCTTCCC	420
TTTATCATTC CAGACCTTGG CAAACTCTA GCTATTAGTT TTATTAGCCG TCCCCTACTT	480
CAACGCCCTTA AAAATCAGGC TTACTTTACT AACTAAAAAA GGATATCGAG TTATCATGAC	540
TCAATATCCT TTTCTTTAT TTGAAACT TATACTCAAT GAAAATCAA GAGCAAACTA	600
GGAAGCTAGC CGCAGGCTnG CAAACACTG TTTGAGGTT GTGGATGAAA CTGACGAGTA	660

1369

AnATCTCATA CATA CGGCAA GGCAAAGCTG AC 692

(2) INFORMATION FOR SEQ ID NO: 354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1005 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

GTGATGGACT ACTGGTTCAA ACCCATCCA	GAAGATTTT TCGATAATGT	CGGACCTCTT	60
GTAGCCAGTA ACTTTTTCA TACTTACACC	GAAGATTTCC ACTTGATGAA	GGAAATTGGA	120
GTAAATTCTT TCCGCACTTC	CATCCAATGG AGTCGACTCA	TCAAGAATTAGAGAC	180
GAGCCTGATC CAAAGGTAT TGCTTCTAC	AATGCCATCA TTGAAGAAC	TAAAAAGAAC	240
CAGATGGATC TTGTGATGAA TTTACATCAT	TTTGATTTAC CAGTGGAACT	TCTTCAAAAA	300
TACGGTGGTT GGGAAAGCAA ACATGTAGTG	GAGTTATTG TGAAAGTTGC	CAAGACTGCT	360
TTCACATGCT TTGGAGATAA GGTTCAATTAC	TGGACAACTT TCAATGAGCC	AATGGTCATT	420
CCAGAACGAG GGTACTTATA TGCTTCCAT	TATCCAATC TAAAAGGAAA	GGGAAAAGAG	480
GCCGTACAAG TCATCTATAA TCTAACCTT	GCTAGTGC	AAAGTGAATTCA	540
TCATTAGAAC TTGATGGAAA GATTGGGATT	ATTTTAAACT TGACACCTGC	TTATCCAAGA	600
AGTAATTCTC CAGAAGACTT AGAAGCAAGT	CGATTTACAG ATGACTTCTT	TAACAAAGTC	660
TTCTTGAAATC CAGCTGTTAA AGGAACCTTC	CCAGAAAGAT TGGTAAACAC	GCTAGAGAGA	720
GATGGCGTGT TATGGAGTCA TACCGAAAAA	GAGCTTCAC	TGATGAAATC AAATACGGTT	780
GATTTCTTG GAGTAAACTA CTACCATCCA	AAACGTGTT	AAGCACAAGC AAATCCTGAG	840
GAATATCAGA CGCCCTGGAT GCCAGACCAA	TACTTCAG	AGTATGAATG GCTGGAGCGT	900
CGCATGAATC CATATCGTGG TTGGGAAATT	TTTCGAAAG	CCATTTATGA TATTGCTATG	960
ATTGTGAAGG AAGAATATGG TAATATCCC	TGGTTTATCA	GTGAA	1005

(2) INFORMATION FOR SEQ ID NO: 355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 973 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

1370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

CCGACAAGCA ATATTAAGGAGTAACTA TTAACCTAGTT AATTAACCGG TTTATTACTT	60
TATAGTGAAT CAAATATACT TAAGAAAAGA GGAAAAGAATG AAAATTAATA AAAATATCT	120
AGCAGGTTCA GTGGCAGTCC TTGCCCTAAG TGTTGTTCC TATGAGCTTG GACGTTACCA	180
AGCTGGTCAG GATAAGAAAG AGTCTAATCG AGTTGCTTAT ATAGATCGTG ATCAGGCTGG	240
TCAAAGGCA GAAAAGTGA CACCAAGATGA AGTCAGTAAG AGGGAGGGGA TCAACGCCGA	300
ACAAATTGTT ATCAAGGTTA CGGATCAAGG TTATGTGACC TCTCATGGAG ACCATTATCA	360
TTACTATAAT GGCAAGGTTTC CTTATGATGC CATCATCAGT GAAGAGCTCC TCATGAAAGA	420
TCCGAATTAT CAGTTGAAGG ATTCAGACAT TGTCATGAA ATCAAGGGTG GTTATGTCAT	480
TAAGGTAAAC CGTAAATACT ATGTTTACCT TAAGGATGCA GCTCATGCCG ATAATATTGCG	540
GACAAAAGAA GAGATTAACAC GTCAGAAGCA GGAACGCACT CATAATCATA ACTCAAGAGC	600
AGATAATGCT GTTGCTGCAG CCAGAGCCCA AGGACGTTAT ACAACGGATG ATGGGTATAT	660
CTTCAATGCA TCTGATATCA TTGAGGACAC GGGTGATGCT TATATCGTTC CTCACGGCGA	720
CCATTACCAT TACATTCCTA AGAATGAGTT ATCAGCTAGC GAGTTAGCTG CTGCAGAAGC	780
CTATTGGAAT GGGAAAGCAGG GATCTCGTCC TTCTTCAGT TCTAGTTATA ATGCAAATCC	840
AGCTCAACCA AGATTTGTCAG AGAACCCACAA TCTGACTGTC ACTCCAACCTT ATCATCAAAA	900
TCAAGGGGAA AACATTTCAA GCCTTTACG TGAATTGAT GCTAACCCCTT ATCAGAACGC	960
CATGTGGGAT CTG	973

(2) INFORMATION FOR SEQ ID NO: 356:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 843 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

GGTCGCATCT GCAATATCTG TCGCCTCCAC ATAAGCGACA CCAGCCTTGT CTGCTGCCCG	60
TTTGACACGT TCTGCAGATT GACCCAGGAT GACCATCTTC TTGAGTCCAG TAATGTCTGG	120
CACCAATTGCG TCAAACCTCAT TGCCACGGTC CAAACCCACCT GCAATCAAGA CGACCTTGCT	180
GTTGTCAAAT CCTGACAAGC TTTTGAGTA GCCAAGATAT TAGTTGATTT ACTGTGTTA	240
TAGAATTAA CACCTTGAT GTCATCCACA AACTGGAGAC GGTGTTGAC ACCACCGAAG	300
GCTGAAAGAG TTTCCTTGAT GCTTTGATTG TCCACATCAC GAAGCTTGGC TACAGCAATA	360

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1371

GTCGCAAGGG CATTTCAC ATTGGCTA CCTGGAACAC CGATTCATT CGCTGCCATG	420
ACTACTCAC CACGGAAGTA GAGTTGACCA TCTTCAGAT AAGCTCCATC AACCTTTCA	480
AGTGTGAAA ATGGTACAAC AGTGGCTCT GTCTTGGAAAG TCAAGTCTTT TGCCAAGTCT	540
TGATTAAGT TCAAGACAAG GAAATCAGCT GCTGTCATCT TGTTCTGGAT ATTCCACTTG	600
GCTGCTACAT ATTCCGAAA TGACCCATGG TAGTCGATAT GAGTTGGCAT GAGGTTGGTA	660
ATAACCGCAA TCTCTGGATG GAATTCTTGA ACACCCATGA GTTGGAAAGA AGAAAGTCC	720
ATAACAAGCG TGTCTTATC TGATGCTATT TGAGCAACCT GACTAGCTGG ATAGCCGATA	780
TTCCCTGATA AAAGACCAGT TTGGCCAGCA GCAGTCAAAA CTTCCCGGn TCCTCTAGAG	840
	843

TCG

(2) INFORMATION FOR SEQ ID NO: 357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 807 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

TTTTTTTTAT ATTTTTTTA TTTATTATTtT TTTGGCAAAA AAGACCAATT TGCTTTGGAG	60
CATTGCTCT GCATTAATT GTCTATTCTT GCTCGTGTG TTACGCTCTT TGTATCATGT	120
ATTAACCTAGC AAGTGCAACT TGCAAACTAC TAGTAAGAGG AGAAAAACAA AATGGTTATG	180
ACTGACCCAA TCGCAGACTT CCTAACTCGT ATTCTAATG CTAACCAAGC TAAACACGAA	240
GTACTTGAAAG TACCTGCATC AAACATCAA AAAGGGATTG CTGAAATCCT TAAACCGGAA	300
GGTTTTGTAA AAAACGTGCA AATCATTGAA GATGACAAAC AAGGCGTCAT CCGTGTATTT	360
CTTAAATACG GACCAAATGG TGAGAAAGTT ATCACTAACT TGAAACGTGT TTCTAAACCA	420
GGACTTCGTG TCTACAAAAA ACGTGAAGAC CTTCCAAAAG TTCTTAACGG ACTTGGAAATT	480
GCCATCCTT CAACCTCTGA AGGTTGCTT ACTGATAAAG AAGCACGCCA AAAGAATGTT	540
GGTGGTGAGG TTATCGCTTA CGTTGGTAA AATCAAGATA CAAAGCTCGT AAAGAACAAA	600
GCAAAATAG GAAGTTGGAG AAGTTGTTT ACAAACAGGC CAACTTATCT ATTTCGACA	660
GTTCTTAGAG CGTGTTCAGT TCAGCTCTG AGCTAAGTAA GTATCTGAAC CCCGTGAAAA	720
CTGGCCGTGC TGGCATGTC GGGTAACAGG AGAAAATAAA CATGTCACGT ATTGGTAATA	780
AGTTCAAGCTA AGGCCTCGT AAAAGTT	807

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(2) INFORMATION FOR SEQ ID NO: 358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 653 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

CCCAGTATT	TTGTCCAAGC	ACGACCAGAA	AAGGATGATA	CAGATCTGGA	ATTGGCTCTC	60
TTAACCATCT	tTGAACAAAA	TCCTCAGGCT	CAGGTCACTA	TTTTCGGTGC	CTTGGGTGGC	120
CGTATTGACC	ATATGTTGGC	CAATGTCTT	CTGCCTAGCA	ATCCTAAGTT	GGCACCCAT	180
ATGCATCAA	TAGAAATTGA	GGATGGGCAA	AACTTGATTA	CTTATTGTCC	AGAAGGAATC	240
AGTCAGCTAG	AACCTCGTTC	AGACTACGAC	TATCTAGCCT	TTATGCCAGT	TCGGGATAGC	300
CAAGTATGAG	TTGACAGAGG	AAAATTTTTT	CTTTAAAAAA	GTGTACGCTT	CTAACGAATA	360
TATAGATAGG	GAAGTGTCGG	TAACTTGCC	AGATGGTTAT	GTGGTCGTAC	TGCATAGCAA	420
GGACAGGAGG	TAGGATGGAA	AGTTTACTTA	TTCTTATTATT	AATTGCCAAT	CTAGCTGGTC	480
TCTTTCTGAT	TTGGCAAAGG	CAGGATAGGC	AGGAGAAACA	CTTAAGTAAG	AGCTTGGAGG	540
ATCAGGCAGA	TCATTTGTCA	GACCAGCTGG	ATTACCGCTT	TGACCAAGCC	AGACAAGCCA	600
GCCAGTTAGA	CCAAAAAGAT	TTGGAAGTGG	TTGTCAAGCGA	CCGTTTGCAA	GAA	653

(2) INFORMATION FOR SEQ ID NO: 359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 641 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

CACCATGTGA	TGTGACGCTG	GCCACAGCTG	TCAGAAATCT	GGCGAGCCAT	CGTGTGCAAT	60
GACTCTTCCC	GAATGTAATCT	TGTTCATAGT	CCTTTGATGA	ATATGTTCAA	GCTGTAGAAG	120
GTGCGCTTCC	TGAACACTTA	TCAACTGTTA	CAGGCGAGTT	GACCGATCAG	GAAACAGATG	180
GCTGGTACAC	ACTTGCCAAC	ACTTCTTCAT	CCCGCATTAA	CCTAAAACAA	GCCTTCCAAG	240
AAAATAGCAA	CCTCCTAGAG	CAAGTGGTAG	AACCCCTGAC	TATTATCACT	GGTGGACACA	300
ACCACAAGGA	CCAGTTGACC	TATGCTTGGA	AAACACTTTT	GCAGAATGCG	CCACATGATA	360
GTATCTGTGG	CTGTAGCGTG	GACGAAGTTC	ACCGCGAGAT	GGAAACCGGT	TTTGCCAAGG	420

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TCAACCAAGT AGGAAACTTT GTTAAAAGTA ACTTGCTCAA CGAGTGGAAAG GGTAAAATTG	480
CTACGGATAA GGCTCAAAGT GACTATCTCT TTACTGTCAT TAACACAGGC TTGCATGATA	540
AGGTCGATAC TGTCAGCACA GTGATTGATG TGGCGACTTG TGATTTCAAG GAATTGCACC	600
CAACAGAAGG CTACAAAAG ATGGCTGCTC TTATCTTGCC G	641

(2) INFORMATION FOR SEQ ID NO: 360:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1958 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

CCTCAAGGCC AATTTGAAGG CTCTAAAACA ATGGAAAAGT GCTACACAGA TGTGACAGAA	60
TTTGCCATTC CAGCAAGTAC TCAAAAGCTT TACTTATCAC CAGTTTTAGA TGGCTTTAAT	120
AGCGAAATTA TTGCTTTAA TCTTTGACT TCACCCAACT TAGAACAGT ACAAACAAATG	180
TTAGAACAGG CATTCAAAGA GAAGCACTAC GAGAACACGA TTCTCCATAG TGACCAAGGC	240
TCCGAAATTC AACACGGATTG TTATCATCGG TTCCCTAGAGA GAAAGGAAAT TCAAGCATCT	300
ATGTCACGCA AGGGCAACAG CCAAGACAAAC GGTATGATGG AATCTTTCTT TGGCATTAA	360
AAATCCGAAA TGTTTTATGG CTATGAGAAA ACATTTAAAT CACTTAACCA ATTGGAAACAA	420
GCCATTATAG ACTATATTGA TTACTACAAAC AACAAACGAA TTAAGGTAAA ACTAAAAGGA	480
CTTAGTCCTG TGCAGTACAG AACTAAATCC TTTGGATAAA TTAATTGTCT AACTTTTTGG	540
GGTCAGTACA AAACTCTTGC TACTATGCGT TTTATTATTG AAAGACTTAT TGGACTTTCT	600
CTCAAATCGA GTTTTTACTC AATTTCTTA CTTGATTGGG ATTGAAATTC CAATTAATT	660
CTCTGAGTAG AGTGTCTTGA TATTGGCTTC ATCAACAGAG GCCTTATCAA TTTTACGTT	720
CAAGAAAAAT TCTTGAATGG TTTCGATTTG AGGCTCACGA ATAGCACGGT CTTTGTGTTGA	780
GATGAGGATT TCATAGTGAA GCGGAGCTTG GGTAAGGATA ACATCTGTAT TCCCTGCAGA	840
ATAAACCTCA ACAAGGGTTG CATCGGTACT TTCTAGCTGA CTTTTTACAA GTTGCAGTG	900
TGAGTTTGTC GTATTGATAA GCTTCATAAT ATTTCCCTCG ATTTTCTAAT TCTATTATAG	960
CACTTTTGAA ATAAAGTCGC TTGATTATAA CTCATGAAA ATCAAAGAGC AACTAGGAA	1020
GCTAGCCGCA GCTATACATT GAGTACGGTA AGGCAGCGCT GACGTGGTT GAATTGTTATT	1080
TTCGAAGAGT ATTAGCCAAT CTTATGCTGT TTTTCCAAG ATTCAATGGC CCATTTATGG	1140

1374	
CTACCACGTT TAAGGTTTT GATAGCCTCG TCAATAGGGA ACCAGGCAAT ATGATTAAG	1200
TTTTCTAGTG GCTTTTGAC TTCTTTGAAA GGAGTTGCTT CATAGAGGTA GGCAGGATTG	1260
TAGTAGTAGG TATCACCGATG ACGAGAAATAG AAATATTCGT CAGCTTGCTC GTAATAGGTA	1320
CCAATTTCTG CTGTGAAACC AAGCTCTTCA ATCAACTCAT GCTTTAGGGC TTCTTGATGA	1380
TTTCACCTG CTTCAATTTC TCCACATGGT AGGAACCAAG CACCATTGG TTCTTGAAACA	1440
AGAACAAATTG TTTTTGTTG AGGATTAGGG ATAACATGCAT ATACGCCATA GCGAGCAATA	1500
TAGTCTGTAT TCACTTTTT TCTCCGAAAG TTGGGTTGC CATTCCATTTC TCCTCATTAT	1560
CTAGTATCGT TATTATTATA GTGAAATGAA CCAAAATAG TACACAATGT GGTATAATCT	1620
TCTTATGGCA TATTCAATAG ATTTTCGTA AAAAGTTCTC TCTTATTGTG AGCGAACAGG	1680
TAGTATAACA GAAGCATCAC ACGTTTCCA AATCTCACGT AATACCATTG ATGGCTGGTT	1740
AAAGCTAAAA GAGAAAACAG GAGAGCTAAA CCACCAAGTA AAAGGAATAA AACCAAGAAA	1800
GGTTGATAGA GATAGACTTA AAAACTATCT TACTGACAAT CCAGACGCTT ATTTGACTGA	1860
AATAGCTTCT GAATTTGGCT GTCATCCAAC TACCATCCAC TATGCGCTCA AAGCTATGGG	1920
tACACTCGAA AAAAAAAAGA ACTACACCTA CTATGAAC	1958

(2) INFORMATION FOR SEQ ID NO: 361:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 851 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

TATGAAATTAA AGTATGATG ATAAAGTTCA GATCTATGAA CTTAGAAAAC AAGGATATA	60
CTTAGAGAAG CTTTCAAATA AATTTGGGAT AAGCAATTCT AATCTTAGGT ATATGATTA	120
ATTGATTGAT CGTTACGGAA TAGAGTTCGT CAAAAAGGA AAAATCGTT ACTATTCTCC	180
TGATTTAAAA CAAGAAATGA TTAATAAAAGT CTGACATGAA GGCTGGACTA AAGATAGAGT	240
TTCTCTTGA TACGGTCTCC CAAGTCGTAC GATACTTCTT AACTGGCTAG CACAATACAG	300
AAAAACGGG TATACTATTG TTGAGAAACC AAGAGGGAGA GTACCTGAGA CGGGAGAATG	360
CCATCCTAAA AAAGTTAAGA GAACTCCGAT TGAAGGAGGA AAAAGGAAA GAAGAAAGAC	420
AGAAATTGTT TAAGAATTAA TGACTGAGTT TTCGTTAGAT CTTCTTTAA AAGTCATTA	480
ACTAGCTCGT TCGACCTACT ACTATCACCTT GAAACAGCTA GATAAAACAG ATAAGGACCA	540
AGAGCTTAAA GCTGAAATTTC AATCCATTTC TATCGAACAC AAAGGAAATT ATGCTTATCG	600

1375

TCGGATTTAT TTAGAACTAA GAAATCGTGG TTATCTGGTA AATCATAAAA GAGTTCAAGG	660
CTTGATGAAA GTACTCAATT TACAAGCTAA AACCGCAGAC AACGAAAAT ATTCTTCTCA	720
TAAAGGAGAC GTTGGCAAGA AGGCAGAGAA TCTCATTCAA GGCCAATTG AAGGCTCTAA	780
AACAATGGAA CAGTGCTACA CAGATGTGAC AGAATTGCC ATTCCAGTAA GTACTTAAA	840
GCTTTACTTA T	851

(2) INFORMATION FOR SEQ ID NO: 362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1168 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

GGGTAGAACG GATATCTCCA ATGAGTTGGT tTAGCTGGTG AAACTGTAAA AAGATTTCGw	60
CCAATTCAAG GTTGAGGCAT CGCAAACAT GGACTGTTTC CTCGTCAGTT CTGGAAAGAA	120
AACGGGATAA GGTTGGCTGT GAAGCAAGCT GCCCTCCTTC CAACAATTAA GGAAAGTAGG	180
CATCAGCTGA CAATTCTTTA CAAGCATAGT CCGTTCCATA ACCTGTTAAC AGTTGAAAGA	240
GGAACTGGAC AAGGATATCT GAATCGAAT AACGACAGTA GCGGCGTTGG TCATTCGTTA	300
CTAAATACTT AGAAATCCGC TCTTTTAGTT TCAACTGGGA AAAAAGTCC TGAAAAAAAGA	360
TAAGACCACC ATACTGGTT AAATGACCTC CATCGAAAGA TAGTTGGTAA AAAGACTTGT	420
TTTGGAAAGTG ATGATTTGGT AAACTGTTCA TGTGAGTTTC CTTCTTTTT GTGTTTTTT	480
CTACACTTAT ACCATAAAGG GGAAACTCTT TTTGTCTAG TAAAAAACAC CCATTGGGTG	540
AAAAAAGAAA CCATCCAGGA TCTAAGCTAA GGCAAGGATT CTGGATGTT TTTAGATTTG	600
GGGTGAATAA TTGGGGTTTT AGCTGCTTGC GCCAATCAG GTTCAGATAC AAAAACTTAC	660
TCATCAACCT TTAGTGGAAA TCCAACATACA TTTAACTATC TATTAGACTA TTACGCTGAT	720
AATATAGTCA ATTGAAACAA GAACAAGACA AAAGAGCCTC ATAAAAGGTA TTGCAACTTG	780
GTAATACCTT TTTGAGGTGC TTTTGATAT GAGCCCATGT TTTCTCAATA GGATTGTACT	840
CAGGTGAGTA GGGAGGAAGA GGTAAAAGTT TATAACCCAAA CTCTTCACAC AAGAGTTCTA	900
ACTTACCCAT TCTATGGAAT CTTGCATTAT CCATAATAAT AACCGATGGT GTGTTAATG	960
TTGGTAAGAG AAATTCTGA AACCAAGCTT CAAAAAAAGTC GCTCGTCATC GTCTCTTCGT	1020
AAGTTATTGG AGCGATTAAC TCACCATTTG TTAGACCTGC AACCAAAGAA ATCCTCTGAT	1080

1376
 ATCTTCTTCC AGATACTTTG CCTCTTCTTA ACTGACCTTT TAATGAGCGA CCATATTCTC 1140
 GATAAAAATA AGTATCGAAT CCTGTTTC 1168

(2) INFORMATION FOR SEQ ID NO: 363:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4483 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

GTCAGCTTCA GCAAGCCCAT CAGCTTCTGA ATCTGCATCA ACCAGTGGT CCGCTTCAGC	60
GTCAACCAGT GCGTCGGCTT CAGCGTCGAC AAGTGCCTCG GCTTCAGCAT CAACGAGTGC	120
GTGGCCTCA GCAAGCGCAA GTACCTCAGC GTCAAGCTTCC GCCTCAACCA GTGCGTCGGC	180
TTCAGCAAGC ACAAGTGGT CAGCCTCAGC AAGTATCTCA GCGTCTGAAT CGGCATCAAC	240
GAGTGGTCT GAGTCAGCAT CAACGAGTAC GTCAAGCTTCA GCAAGCACAT CAGCTTCTGA	300
ATCTGCATCA ACCAGTGGT CAGCCTCAGC ATCGACAAGC GCCTCAGCTT CAGCAAGTAC	360
CAGTGCTTCA GCCTCAGCGT CGACAAGTGC GTGGCCTCA ACCAGTGCAT CTGAATCGGC	420
ATCAACCAGT GCGTCAGCCT CAGCAAGTAC TAGTGCATCA GCTTCAGCAT CAACGAGTGC	480
ATCGGCTTCA GCATCAACCA GTGCCCGGC TTCAGCGTCA ACCAGTGGT CAGCTTCAGC	540
AAGTACCAAGT GCTTCAGTCT CAGCATCAAC AAGTGCCTCA GCCTCAGCAT CGACAAGTGC	600
CTCGGCTTCA GCAAGCACAT CAGCATCTGA ATCAGCGTCA ACAAGCGCCT CAGCTTCAGC	660
AAGTACCAAGT GCGTCAGCCT CAGCGTCGAC AAGTGCCTCA GCCTCAGCAA GTACTAGTGC	720
ATCAGCTTCA GCATCAACGA GTGCATCGGC TTCAGCGTCA ACCAGTGCAT CAGAGTCAGC	780
AAGTACCAAGT GCGTCAGCTT CCGCATCAAC AAGTGCCTCG GCTTCAGCAA GCACCAAGTGC	840
CTCGGCTTCA GCAAGTACTA GCGCCTCAGC CTCAGCTTCA ACCAGTGGT CAGCCTCAGC	900
AAGTATCTCA GCGTCTGAAT CGGCATCAAC GACTGCGTCC GCTTCAGCAA GTACTAGCGC	960
CTCAGCCTCA GCGTCAACAA GTGCATCGGC TTCAGCGTCA ACGAGTGGT CTGAATCGGC	1020
ATCAACGAGT GCGTCCGCTT CAGCAAGTAC TAGCCTTCA GCCTCAGCGT CAACAAGTGC	1080
ATCGGCTTCA GCATCAACGA GTGCGTCCGC TTCAGCAAGT ACTAGCGCCT CAGCCTCAGC	1140
GTCAACAAAGT GCATCGGCTT CAGCGTCAAC GAGTGCCTCT GAGTCAGCAT CAACGAGTGC	1200
GTCAGCCTCA GCAAGCACAT CAGCTTCTGA ATCTGCATCA ACCAGTGGT CAGCCTCAGC	1260
ATCGACAAGC GCCTCAGCTT CAGCAAGTAC CAGTGCCTCA GAGTCAGCGTC GACAAGTGCs	1320

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TCrGCTTCAG	CAAGTACCAAG	TGCGTCAGCC	TCAGCAAGTA	CCAGTGCKTC	AGCCTCAGCG	1380
TCGACAAGTG	CCTCGGCCTC	AACCAGTGCA	TCTGAATCGG	CATCAACCAG	TGCGTCAGCC	1440
TCAGCAAGTA	CTAGCGCCTC	AGCCTCAGCA	TCAACGAGTG	CGTCGGCTTC	AGCAAGTACT	1500
AGTGCATCAG	CTTCAGCAAG	TACTAGCGCC	TCAGCCTCAG	CGTCGACAAG	CGCCTCAGCT	1560
TCAGCAAGTA	CCAGTGCGTC	AGCCTCAGCG	TGCGACAAGTG	CGTCGGCTTC	AGCAAGTACC	1620
TCAGCGTCTG	AATCAGCATH	AACAAGTGCG	TCGGCTTCAG	CATCAACGAG	TGCATCAGCT	1680
TCAGCATCAA	CAAGTGCTTC	AGCTTCAGCA	AGTACCAAGTG	CGTCGGCTTC	AGCATCAACG	1740
AGTGCCTTCAG	TCTCAGCGTC	AACCAGTGCC	TCTGAATCCG	CATCAACAAG	TGCCTCGGCT	1800
TCAAGCAAGCA	CCAGTGCTTC	GGCTTCAGCG	TCAACGAGTG	CGTCTGAGTC	AGCATCAACG	1860
AGTGGTCAAC	CTCAGCAAGC	ACATCAGCTT	CTGAATCTGC	ATCAACCAAGT	GCGTCACTTC	1920
CGCATCAACA	AGGCCTCGG	CCTCAGCAAG	TACAAGTGCT	TCAGCCTCAG	CATCAACCAG	1980
TGCAATCAGCT	TCAGCCTCAA	CAAGTGCTTC	AGCCTCAGCG	TCAACCAGTG	CCTCGGCTTC	2040
AGCAAGTACC	AGTGGTCAAG	CACAAGTGCG	TCAGCTTCAG	CATCAACCAG	2100	
TGCTTCGGCT	TCGGCATCAA	CAAGTGCCCTC	AGCATCAGCA	TCAACGAGTG	CGTCAsCTCA	2160
GCAAGTACTA	GTGCATCAGC	ATCAGCATCA	ACCAGTGCAT	CAGCCTCAGC	AAGTATCTCA	2220
GCGCTGAAT	CGGCATCAAC	GAGTGCATCA	GCATCAGCAT	CAACGAGTGC	ATCGGCTTCA	2280
GCGTCAACCA	GTGCATCAGT	CTCAGCAAGC	ACCAGTGCCTG	CGGCTTCAGC	ATCAACCAAGT	2340
GCCTCAGCCT	CAGCAAGTAT	CTCAGCGTCT	GAATCGGCAT	CAACGAGTGC	GTCAGCCTCA	2400
GCAAGTACTA	GTGCATCAGC	ATCAGCATCA	ACGAGTGCAT	CGGCTTCAGC	AAGTACCAAGC	2460
GCCTCAGCCT	CAGCAAGCAC	CAGTGCCTCA	GCCTCAGCAA	GTACCAGCGC	CTCAGCCTCA	2520
GCAACCA	GTGCCTCAGC	TTCAGCAAGT	ACCAGTGCCTG	CAGCCTCAGC	GTCGACAAGT	2580
GCGTCGGCTT	CAGCAAGTAC	CTCAGCGTCT	GAATCAGCAT	CAACGAGTGC	ATCAGCTTCA	2640
GCATCAACAA	GTGCCTCAGC	TTCAGCAAGT	ACCAGTGCCTG	CGGCTTCAGC	ATCAACCAAGT	2700
GCTTCAGTCT	CAGCGTCAAC	CAGTGCCTCT	GAATCAGCAT	CAACAAGTGC	CTCGGCTTCA	2760
GCAAGCACCA	GTGCCTCGGC	TTCAGCAAGT	ACTAGTGCAT	CGGCTTCAGC	ATCGACAAGT	2820
GCGCTGAAT	CGGCATCAAC	GAGTGCCTCG	GCTTCAGCAT	CAACGAGTGC	GTCAGCCTCA	2880
GCAAGCACAT	CAGCTTCTGA	ATCTGCATCA	ACCAGTGCCTG	CGGCTTCAGC	GTCAACCAAGT	2940
GCGTCGGCTT	CAGCGTCAAC	AAAGTGCCTCG	GCTTCAGCAT	CAACGAGTGC	GTCGGCCTCA	3000
GCAAGGCCAA	GTACCTCAGC	GTCAGCTTCC	GCCTCAACCA	GTGCCTCCGC	TTCAGCAAGC	3060

1378	
ACAAGTGCCT CAGCCTCAGC AAGTATCTCA GCGTCTGAAT CGGCATCAAC GAGTGGCTCG	3120
GCCTCAGCAA GCGCAAGTAC CTCAGCGTCA GCTTCCGCCT CAACCAAGTGC GTCGGCTTCA	3180
GCAAGCACAA GTGCCTCAGC CTCAGCAAGT ATCTCAGCGT CTGAATCGGC ATCAACGAGT	3240
GCGTCTGAGT CAGCATCAAC GAGTACGTCA GCCTCAGCAA GCACATCAGC TTCTGAATCG	3300
GCATCAACCA GTGCCTCAGC CTCAGCATCG ACAAGCGCCT CAGCTTCAGC AAGTACCAAGT	3360
GCTTCAGCCT CAGCGTCGAC AAGTGGCTCG GCCTCAACCA GTGCATCTGA ATCGGCATCA	3420
ACCAGTGCCT CAGCCTCAGC AAGTACTAGT GCATCAGCTT CAGCATCAAC GAGTGCATCG	3480
GCTTCAGCAT CAACCAAGTGC CTCGGCTTCA GCGTCAACCA GTGCCTCAGC TTCAGCAAGT	3540
ACCAGTGCCTT CAGTCTCAGC ATCAACAAAGT GCTTCAGCCT CAGCATCGAC AAGTCCCTCG	3600
GCTTCAGCAA GCACATCAGC ATCTGAATCA GCGTCGACAA GCGCCTCAGC TTCAGCAAGT	3660
ACCAGTGCCT CAGCCTCAGC GTCGACAAAGT GCGTCAGCCT CAGCAAGTAC TAGTGCATCA	3720
GCTTCAGCAT CAACGAGTGC ATCGGCTTCG GCGTCAACCA GTGCATCAGA GTCAGCAAGT	3780
ACCAGTGCCT CAGCTTCCGC ATCAACAAAGT GCCTCGGCTT CAGCAAGCAG CAGTGGCTCG	3840
GCTTCAGCAA GTACTAGCGC CTCAGCCTCA GCCTCAACCA GTGCCTCAGC CTCAGCAAGT	3900
ATCTCAGCGT CTGAATCGGC ATCAACAGGT GCGTCCGCTT CAGCAAGTAC TAGGCGCTCA	3960
GCCTCAGCGT CAACAAAGTGC ATCGGCTTCA GCGTCAACGA GTGCCTCTGA ATCGGCATCA	4020
ACGAGTGCCT CCGCTTCAGC AAGTACTAGC GCCTCAGCCT CAGCGTCAGC AAGTGCATCG	4080
GCTTCAGCAT CAACGAGTGC GTCCGCTTCA GCAAGTACTA GCGCCTCAGC CTCAGCGTCA	4140
ACAAGTGCAT CCGGTTTCAGC GTCAACAGGT GCGTCTGAGT CAGCATCAAC GAGTGGCTCA	4200
CCTCAKCAAG CACATCAGCT TCTGAATCTG CATCAACCAAG TGCGTCACTT CCGCATCAAC	4260
AAGCGCCTCG GCCTCAGCAA GTACAAGTGC TTCAGCCTCA GCATCAACCA GTGCATCAGC	4320
TTCAGCCTCA ACAAGTGCCTT CAGCCTCAGC GTCAGACCAAG TGCGCTGGCT TCAGCAAGTA	4380
CCAGTGGCTC ACTTCAGCAA GCACAAGTGC GTCAGCTTCA GCATCAACCA GTGCTTCGGC	4440
TTCGGCATCA ACAAGTGCCT CAGCATCAGC ATCAACAGGT GCG	4483

(2) INFORMATION FOR SEQ ID NO: 364:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2550 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

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GTACCTCAGC	GTCCCTCCGC	CTCAACCAGT	GCGTCCGCTT	CAGCAAGCAC	AAGTGCCTCA	60
CCTCAGCAAG	TATCTCAGCG	TCTGAATCGG	CATCAACGAG	TGGCTCGGCC	TCAGCAAGCG	120
CAAGTACCTC	AGCGTCACCTT	CCGCCTCAAC	CAGTGCCTCG	GCTTCAGCAA	GCACAAGTGC	180
GTCAsCTCAG	CAAGTATCTC	AGCGTCTGAA	TCGGCATCAA	CGAGTGCCTC	TGAGTCAGCA	240
TCAACGAGTA	CGTCAGCCTC	AGCAAGCAC	TCAGCTCTG	AATCGGCATC	AACCAGTGCG	300
TCAGCCTCAG	CATCGACAAG	CGCCTCAGCT	TCAGCAAGTA	CCAGTGCCTC	AGCCTCAGCG	360
TCGACAAGTG	CGTCGGCCTC	AACCAGTGCA	TCTGAATCGG	CATCAACCAG	TGGCTCAGCC	420
TCAGCAAGTA	CTAGTCATC	AGCTTCAGCA	TCAACGAGTG	CATCGGCCTC	AGCATCAACC	480
AGTGCCTCGG	CTTCAGCGTC	AACCAGTGCG	TCAGCTTCAG	CAAGTACCAAG	TGCTTCAGTC	540
TCAGCATCAA	CAAGTGCTTC	AGCCTCAGCA	TCGACAAGTG	CCTCGGCTTC	AGCAAGCACA	600
TCAGCATCTG	AATCAGCGTC	GACAAGTGCG	TCGGCCTCAA	CCAGTGCATC	TGAATCGGCA	660
TCAACCAAGTG	CGTCAGCCTC	AGCAAGTACT	AGTGCATCAG	CTTCAGCCTC	AACGAGTGCA	720
TCGGCTTCGG	CCTCAACCAAG	TGCATCAGAG	TCAGCAAGTA	CCAGTGCCTC	AGCTTCGGCA	780
TCAACAAAGTG	CCTCGGCTTC	AGCAAGCAC	TCAGCATCTG	AATCAGCGTC	AACCAGTGCT	840
TCGGCTTCAG	CAAGTACCAAG	TGCTTCAGCT	TCAGCATCAA	CCAGCCTCCTC	GGCCTCAGCA	900
AGCACCTCAG	CTTCTGAATC	GGCCTCAACC	AGGCCTCAGG	CCTCAGCAAG	CACCTCAGCT	960
TCTGAATCGG	CCTCAACCAAG	CGCCTCAGCC	TCAGCATCAA	CGAGTGCCTC	GGCTTCAGCA	1020
AGCACAAAGCG	CCTCGGGTTC	AGCATCAACG	AGTACGTCAG	CTTCAGCGTC	AACCAGTGCT	1080
TCAGCCTCAG	CATCAACAAG	TGCGTCAGCC	TCAGCAAGTA	TCTCAGCGTC	TGAATCGGCA	1140
TCAACGAGTG	CGTCTGAGTC	AGCATCAACG	AGTACGTCAG	CCTCAGCAAG	CACAAGTGCT	1200
TCAGCCTCAG	CAACTATCTC	AGCGTCTGAA	TCGGCATCAA	CGAGTGCCTC	CGCTTCAGCA	1260
AGTACTAGCG	CCTCAGCCTC	AGCGTCAACA	AGTGCTTCGG	CTTCAGCGTC	AACGAGTGCG	1320
TCTGAGTCAG	CATCAACGAG	TACGTCAGCC	TCAGCAAGCA	CATCAGCTTC	TGAATCTGCA	1380
TCAACCAGTG	CGTCAGCCTC	AGCATCGACA	AGCGCCTCAG	CTTCAGCAAG	TACCAAGTGC	1440
TCAGCCTCAG	CAAGTACCAAG	TGCTTCAGCC	TCAGCGTCGA	CAAGTGCCTC	GGCCTCAACC	1500
AGTGCATCTG	AATCGGCATC	AACCAGTGCG	TCAGCTCAGC	AAGTACTAGT	GCATCAGCTT	1560
CAGCATCAAC	GAGTGCATCG	GCTTCGGCGT	CAACCAAGTGC	ATCAGAGTCA	GCAAGTACCA	1620
GTGCGTCACT	TCCGCATCAA	CAAGTGCCTC	GGCTTCAGCA	AGCACATCAG	CATCTGAATC	1680
AGCGTCAACC	AGTGCCTCGG	CTTCAGCAAG	TACCAAGTGC	TCAGCTTCAG	CATCAACCAG	1740

1380	
CGCCTCGGCC TCAGCAAGCA CCTCAGCTTC TGAATCGGCC TCAACCAGCG CCTCGGCCCTC	1800
AGCAAGCACC TCAGCTTCTG AATCGGCCTC AACCAAGCGCC TCAGCCTCAG CATCAACGAG	1860
TGCTTCGGCT TCAGCAAGCA CAAGCGCCTC GGGTCAGCA TCAACGAGTA CGTCAGCTTC	1920
AGCGTCAACC AGTGCCTCAG CCTCAGCATC AACAAAGTGC GTCAGCCTCAG CAAGTATCTC	1980
AGCGTCTGAA TCGGCATCAA CGAGTGCCTC TGAGTCAGCA TCAACGAGTA CGTCAGCCTC	2040
AGCAAGCACC TCAGCTTCTG AATCGGCCTC AACCAAGTGC GTCAGCCTCAG CATCGACAA	2100
CGCCTCAGCT TCAGCAAGTA CCAGTGCTTC AGCCTCAGCG TCGACAAGTG CGTCGGCCTC	2160
AACCAAGTGCA TCTGAATCGG CATCAACCAAG TGCGTCAGCC TCAGCAAGTA CTAGTGCATC	2220
GGCTTCAGCA TCAACCAGTG CCTCGGCCTC AGCGTCAACC AGTGCCTCAG CTTCAGCAAG	2280
TACCAAGTGCT TCAGTCTCAG CATCAACAAG TGCTTCAGCC TCAGCATCGA CAAGTGCCTC	2340
GGCTTCAGCA AGCACATCAG CATCTGAATC AGCGTGCACA AGCGCCTCAG CTTCAGCAAG	2400
TACCAAGTGCG TCAGCCTCAG CGTCGACAAG TCGCTCAGCT ACAGCAAGTA CTAGTGCATC	2460
AGCTTCAGCA TCAACGAGTG CATCGGCCTC GCGTCAACC AGTGCATCAG AGTCAGCAAG	2520
TACCAAGTGCG TCAGTTCACG CATCAACAAG	2550

(2) INFORMATION FOR SEQ ID NO: 365:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1436 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

ACCCAGCAAG TACTAGTGCA TCGGCTTCAG CAAGCACCAG TGCCTCGGCT TCAGCATCAA	60
CCAGTGCCTC AGCCTCAGCA AGTATCTCAG CGTCTGAATC GGCATCAACG AGTGCCTCAC	120
CTCAGCAAGT ACTAGTGCAT CAGCATCAGC ATCAACGAGT GCATCGGCTT CAGCAAGTAC	180
CAGCGCCTCA GCTTCAGCAA GCACCAAGTGC GTCAsCTCAG CAAGTACCGAG CGCCTCAGCC	240
TCAGCAAGCA CCAGTGCTC AGCTTCAGCA AGTACCAAGTG CGTCAGCCTC AGCGTGCACA	300
AGTGCCTCGG CTTCAGCAAG TACCTCAGCG TCTGAATCAG CATCAACGAG TGCATCAGCT	360
TCAGCATCAA CAAGTGCTTC AGCTTCAGCA AGTATCTCAG CGTCTGAATC GGCATCAACG	420
AGTGCCTCGG CTTCAGCAAG TACTAGGCC TCAGCATCAG CGTCAACAAAG TGCTTCGGCT	480
TCAGCGTCAA CGAGTGCCTC TGAGTCAGCA TCAACGAGTA CGTCAGCCTC AGCAAGCACA	540
TCAGCTTCTG AATCTGCATC AACCAAGTGC GTCAGCCTCAG CATCGACAAAG CGCCTCAGCT	600

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TCAGCAAGTA CCAGTGGTC AgCCTCAGCA AGTACCAAGTG CTTCAAGCCTC AGCGTCGACA	660
AGTGGCGTCGG CCTCAACCGAG TGCATCTGAA TCGGCATCAA CCAGTGGTCGTC AGCCTCAGCA	720
AGTACTAGCG CCTCAGCCTC AGCATCAACG AGTGGCGTCGG CTTCAAGCAAG TACTAGTGCA	780
TCAGCTTCAG CAAGTACTAG CGCCTCAGCC TCAGCGTCGA CAAGCGCCTC AGCTTCAGCA	840
AGTACCAAGTG CGTCAGCCTC AGCGTCGACA AGTGGCGTCGG CTTCAAGCAAG TACCTCAGCG	900
TCTGAATCAG CATCAACAAG TGCCTCGGCT TCAGCATCAA CGAGTGCATC AGCTTCAGCA	960
TCAACAAGTG CTTCAAGCTTC AGCAAGTACC AGTGGCGTCGG CTTCAAGCCTC AACGAGTGCT	1020
TCAGTCTCAG CGTCAACCGAG TGCCTCTGAA TCCGCATCAA CAAGTGCCTC GGCTTCAGCA	1080
AGCACCAGTG CTTCGGGCTTC AGCGTCAACG AGTGGCGTCGG AGTCAGCCTC AACGAGTGCG	1140
TCAGCCTCAG CAAGCACATC AGCTTCAGGAA TCTGCATCAA CCAGTGCCTC AGCTTCAGCA	1200
TCAACAAGCG CCTCGGGCTC AGCAAGTACA AGTGGCTTCAG CCTCAGCCTC AACCAAGTGCA	1260
TCAGCTTCAG CCTCAACAAG TGCTTCAGCC TCAGCGTCAA CCAGTGCCTC GGCTTCAGCA	1320
AGTACCAAGTG CGTCAGCTTC AGCAAGCACA AGTGGCGTCAG CTTCAAGCCTC AACCAAGTGCT	1380
TCGGCTTCAGG CATCAACAAG TGCCTCAGCA TCAGCATCAA CGAGTGCCTC AGCCGG	1436

(2) INFORMATION FOR SEQ ID NO: 366:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 735 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

GCAGTGTGCCA CACCGTGCTG ACCAGCACCC GTTCCCTGGCA TAATTTTCTT TTTACCCATG	60
CGTwtGGCAA GCCAAACTTG TCCTAAAGGCA TTGTTAACCT TGTTGGCTCC TGATGGTTA	120
AGGTCTTCCC GTTTGAGATA AATCTTGCTC CGCCAATATG CTGGGTCAAG TTTTTGCGT	180
AATAAAAGAGG AGTTTCACGT CCTACGTACT GGCGCAAAAG CTGGTTTAAT TCCTCTTGGA	240
AACTTGGTC TCCCTGACTT TCACGGTAGG CCTTCTCCAA CTCCAAAATCT GCTGTCTCA	300
ATGTTTCTGG GACAAAACGT CGGCCGAATT TTCCGTAAAA TCCATCTTTA TTTGGTTCCCT	360
GATATGCCAT GCTTACCCCT CTCTATAAAT CTCTAACCT TTTCATGATC TTTTTGTCCA	420
TCTGTCTCCA CTCCGCTCGA TACATCTACT GCATAGGGAG TAAAGTGTG AATTGCTTTT	480
ACTACATTAT CTTCAATTAG GCCACCTGCG ATAAGAAGG GCTGTGCTAG TCCAGTCGTA	540

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TCAGGTGAC CCCAATCAA GGGCTGGCA CTTCCCTGCCA CAGGGGCATC AAAGAGTAGA	600
TAATCTGCCT GAGAATTGGG GACATGCCA TTTCCATCTA CCTGCACAGC CTGAATACTG	660
GCACAAGGCA AATTCTCAA TAAATCATCT GCCACCTGAC CGTGAACCTG AACCAAGTCC	720
AAGCCGGGGA TCCTC	735

(2) INFORMATION FOR SEQ ID NO: 367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1702 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

TACTAGCGCC TCAGCCTCAG CGTCAACAAG TGCATCGGCT TCAGCATCAA CGAGTGCCTC	60
CGCTTCAGCA AGTACTAGCG CCTCAGCCTC AGCGTCAACA AGTGCATCGG CTTCAGCGTC	120
AACGAGTGCAG TCTGAGTCAG CATCAACGAG TCGCTCAGCC TCAGCAAGCA CATCAGCTTC	180
TGAATCTGCA TCAACCAGTG CGTCAGCCTC AGCATCGACA AGGCCTCAG CTTCAGCAAG	240
TACCAAGTGCAG TCAGCCTCAG CGTCGACAAG TGCCTCGGCT TCAGCAAGTA CCAGTGCCTC	300
AGCCTCAGCA AGTACCAAGTG CGTCAGCCTC AGCGTCGACA AGTGCCTCGG CCTCAACCAG	360
TGCATCTGAA TCGGCATCAA CCAGTGCCTC AGCCTCAGCA ACTACTACTG CATCAGCTTC	420
AGCATCAACG AGTGCATCGG CTTCAGCCTC AACCAAGTGCAG TCAAGTGCAG CAAGTACCAAG	480
TGCGTCAGCT TCCGCATCAA CAAGTGCCTC GGCTTCAGCA AGTACTAGCG CCTCAGCCTC	540
AGCGTCAACA AGTGCCTCAG CTTCCCGCTC AACCAAGCCTC TCGGCCTCAG CAAGTATCTC	600
AGCGTCTGAA TCGGCATCAA CAAGTGCCTC GGCTTCAGCA TCAACAGAGTG CATCAGCTTC	660
AGCAAGCACC AGTGCCTCGG CCTCAGCAAG CACCAGCGCG TCTGAATCCG CATCAACCAG	720
TGCGCTCAGCT TCAGCAAGTA CCTCAGCCTC TGAATCAGCA TCAACAAAGTG CATCGCTTC	780
AGCAAGCACA AGTGCCTCAG CCTCAGCAAG TATCTCAGCG TCTGAATCCG CATCAACGAG	840
TGCGTCAGCT TCAGCAAGTA CTAGCCTCAG CCTCAGCCTC AGCATCAGCG TCAACAAAGTG CTTCAGCTTC	900
AGCGTCAACG AGTGCCTCAG AGTCAGCCTC AACCAAGTGCAG TCAGCCTCAG CAAGCACATC	960
AGCTTCTGAA TCTGCATCAA CCAGTGCCTC AGCCTCAGCA TCGACAAGCG CCTCAGCTTC	1020
AGCAAGTACG AGTGCCTCAG CCTCAGCAAG TACCAAGTGCAG TCAGCCTCAG CGTCGACAAG	1080
TGCGTCAGCT TCAACCAGTG CATCTGAATC GGCAATCAAAG AGTGCCTCAG CCTCAGCAAG	1140
TACTAGCGCC TCAGCCTCAG CATCAACGAG TGCCTCCGCT TCAGCAAGTA CTAGCCTCAG	1200

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AGCATCAGCA TCAACGAGTG CATCGGCTTC AGCAAGTACC AGCGCCTCAG CTTCAGCAAG	1260
CACCACTGCG TCAGCCTCAG CAAGTACCAAG CGCCTCAGCC TCAGCAAGCA CCAGTGCCTC	1320
AGCTTCAGCA AGTACCAAGTG CGTCAGCCTC AGCGTCGACA AGTGCCTCGG CTTCAGCAAG	1380
TACCTCAGCG TCTGAATCAG CATCAACGAG TGCAATCAGCT TCAGCATCAA CAAGTGCCTC	1440
AGCTTCAGCA AGTACCAAGTG CGTCGGCTTC AGCATCAACG AGTGCCTCAG TCTCAGCGTC	1500
AACCACTGCC TCTGAATCAG CATCAACAAG TGCCTCGGCT TCAGCAAGCA CCAGTGCCTC	1560
GGCTTCAGCA AGTACTAGTG CATCGGCTTC AGCATCGACA AGTGCCTCTG AATCGGCATC	1620
AACGAGTGCT TCGGCTTCAG CATCAACGAG TGCCTCAGCC TCAGCAAGCA CATCAGCTTC	1680
TGAATCTGCA TCAACCAAGTG CG	1702

(2) INFORMATION FOR SEQ ID NO: 368:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 941 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

ACCAGTGCAT CAGCTTCAGC CTCAACAAGT GCTTCAGCCT CAGCGTCAAC CAGTGCCTCG	60
GCTTCAGCAA GTACCAAGTG GTCACCTCAG CAAGCACAAG TGCGTCACCT CAGCATCAAC	120
CAGTGCTTCG GCTTCGGCAT CAACAAGTGC CTCAGCATCA GCATCAACGA GTGCCTCACC	180
TCAGCAAGTA CTAGTGCATC AGCATCAGCA TCAACCAAGTG CATCAGCCTC AGCAAGTATC	240
TCAGCGTCTG AATCGGCATC AACGAGTGCA TCAGCATCAG CATCAACGAG TGCAATCGGCT	300
TCAGCGTCAA CCAGTGCATC AGTCTCAGCA AGCACCAAGTG CGTCGGCTTC AGCATCAACG	360
AGTGCCTCAG CCTCAGCAAG TATCTCAGCG TCTGAATCGG CATCAACGAG TGCGTCAGCC	420
TCAGCAAGTA CTAGTGCATC GGCTTCAGCA AGCACCAAGTG CGTCGGCTTC AGCATCAACC	480
AGTGCCTCAG CCTCAGCAAG TATCTCAGCG TCTGAATCGG CATCAACGAG TGCGTCAGCC	540
TCAGCAAGTA CTAGTGCATC AGCATCAGCA TCAACGAGTG CATCGGCTTC AGCAAGTACC	600
AGCGCCTCAG CTTCAAGCAAG CACCAAGTGC CGTCAGCCTCAG CAAGTACCAAG CGCCTCAGCC	660
TCAGCAAGCA CCAGTGCCTC AGCTTCAGCA AGTACCAAGTG CGTCAGCCTC AGCGTCGACA	720
AGTGCCTCGG CTTCAAGCAAG TACCTCAGCG TCTGAATCAG CATCAACGAG TGCAATCAGCT	780
TCAGCATCAA CAAGTGCCTC AGCTTCAGCA AGTACCAAGTG CGTCGGCTTC AGCATCAACG	840

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

CCGACAAGCA ATATTAAGGAA GAGTAACTA TAACTAGTT AATTAACCGG TTTATTACTT	60
TATAGTGAAT CAAATATACT TAAGAAAAGA GGAAAAGAATG AAAATTAATA AAAATATCT	120
AGCAGGTTCA GTGGCAGTCC TTGCCCTAAG TGTTGTTCC TATGAGCTTG GACGTTACCA	180
AGCTGGTCAG GATAAGAAAAG AGTCTAATCG AGTTGCTTAT ATAGATGGTG ATCAGGCTGG	240
TCAAAGGCA GAAAAGCTGA CACCAAGATGA AGTCAGTAAG AGGGAGGGGA TCAACGCCGA	300
ACAAATTGTT ATCAAGAGTTA CGGATCAAGG TTATGTGACC TCTCATGGAG ACCATTATCA	360
TTACTATAAT GGCAGGGTTC CTTATGATGC CATCATCAGT GAAGAGCTCC TCATGAAAGA	420
TCCGAATTAT CAGTTGAAGG ATTCAAGACAT TGTCATGAA ATCAAGGGTG GTTATGTCAT	480
TAAGGTAAAC GGTAAATACT ATGTTTACCT TAAGGATGCA GCTCATCCGG ATAATATTG	540
GACAAAAGAA GAGATTAAC GTCAGAAGCA GGAACGCAGT CATAATCATA ACTCAAGAGC	600
AGATAATGCT GTTGCTGCAG CCAGAGCCCA AGGACGTTAT ACAACGGATG ATGGGTATAT	660
CTTCAATGCA TCTGATATCA TTGAGGACAC GGGTGATGCT TATATCGTTC CTCACGGCGA	720
CCATTACCAT TACATTCTA AGAATGAGTT ATCAGCTAGC GAGTTAGCTG CTGCAGAAC	780
CTATTGGAAT GGGAAAGCAGG GATCTCGTCC TTCTTCAAGT TCTAGTTATA ATGCAAATCC	840
AGCTCAACCA AGATTGTCAG AGAACCCACAA TCTGACTGTC ACTCCAACCTT ATCATCAAAA	900
TCAAGGGGAA AACATTTCAGA GCCTTTACG TGAATTGTAT GCTAACCTT ATCAGAACGC	960
CATGTGGGAT CTG	973

(2) INFORMATION FOR SEQ ID NO: 356:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 843 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

GGTCGCATCT GCAATATCTG TCGCCTCCAC ATAAGCGACA CCAGCCTTGCT CTGCTGCCG	60
TTTGACACGT TCTGCAGATT GACCCAGGAT GACCATCTTC TTGAGTCCAG TAATGTCTGG	120
CACCAATTCTG TCAAACATCAT TGCCACGGTC CAAACCCACCT GCAATCAAGA CGACCTTGCT	180
GTTGTCAAAT CCTGACAAGC TTTTGAGTA GCCAAGATAT TAGTTGATTT ACTGTGTTA	240
TAGAATTCAA CACCTTGAT GTCATCCACA AACTGGAGAC GGTGTTGAC ACCACCGAAG	300
GCTGAAAGAG TTTCCTTGAT GGTTTGATG TCCACATCAC GAAGCTTGGC TACAGCAATA	360

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1371	
GTCGCAAGGG CATTTCAC ATTGTGGCTA CCTGGAACAC CGATTCATT CGCTGCCATG	420
ACTACTCAC CACGGAAAGTA GAGTTGACCA TCTTCCAGAT AAGCTCCATC AACCTTTCA	480
AGTGTGAAA ATGGTACAAC AGTGGCTTCT GTCTTGGAAAG TCAAGTCTTT TGCCAAGTCT	540
TGATTAAGT TCAAGACAAG GAAATCAGCT GCTGTCATCT TGTTCTGGAT ATTCCACTTG	600
GCTGCTACAT ATTCCGAAA TGACCCATGG TAGTCGATAT GAGTTGGCAT GAGGTTGGTA	660
ATAACCGAA TCTCTGGATG GAATTCTTGA ACACCCATGA GTTGGAAAGA AGAAAAGTCC	720
ATAACAAGCG TGTCTTATC TGATGCTATT TGAGCAACCT GACTAGCTGG ATAGCCGATA	780
TTCCCTGATA AAAGACCAGT TTGGCCAGCA SCAGTCAAA CTTCCCGGn TCCTCTAGAG	840
	843

TCG

(2) INFORMATION FOR SEQ ID NO: 357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 807 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:	
TTTTTTTTAT ATTTTTTTTA TTTATTATT TTTGGCAAAA AAGACCAATT TGCTTTGGAG	60
CATTGCTCT GCATTAATT GTCTATTCTT GCTCGTGCCTG TTACGCTCTT TGTATCATGT	120
ATTAACTAGC AAGTGCACT TGCAAACTAC TAGTAAGAGG AGAAAACAA AATGGTTATG	180
ACTGACCCAA TCGCAGACTT CCTAACTCGT ATTGTAATG CTAACCAAGC TAAACACGAA	240
GTACTTGAAG TACCTGCATC AAACATCAA AAAGGGATTG CTGAAATCCT TAAACCGAA	300
GGTTTTGTAA AAAACGTGA AATCATTGAA GATGACAAAC AAGGCGTCAT CCGTGTATTT	360
CTTAAATACG GACCAATGG TGAGAAAGTT ATCACTAACT TGAAACGTGT TTCTAAACCA	420
GGACTTCGTG TCTACAAAAA ACGTGAAGAC CTTCCAAAAG TTCTTAACGG ACTTGGAAATT	480
GCCATCCTT CAACTCTGA AGGTTTGCTT ACTGATAAG AAGCACGCCA AAAGAATGTT	540
GGTGGTGAGG TTATCGCTTA CGTTGGTAA AATCAAGATA CAAAGCTCGT AAAGAACAAA	600
GTTCTTAGAG CGTGTTCAGT TCAGCTCTG AGCTAAGTAA GTATCTGAAC CCCGTGAAAA	660
CTGGCCGTGC TGGCATGGTC GGGTAACAGG AGAAATAAA CATGTCACGT ATTGGTAATA	720
AGTTCAGCTA AGGCCTTCGT AAAAGTT	780
	807

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(2) INFORMATION FOR SEQ ID NO: 358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 653 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

CCCACTATTT TTGTCCAAGC ACGACCAGAA AAGGATGATA CAGATCTGGA ATTGGCTCTC	60
TTAACCATCT TTGAAACAAAAA TCCTCAGGCT CAGGTCACTA TTTTCGGTGC CTTGGGTGGC	120
CGTATTGACC ATATGTTGGC CAATGTCTTT CTGCCTAGCA ATCCTAAGTT GGCACCCAT	180
ATGCATCAA TAGAAATTGA GGATGGGCAA AACCTTGATTA CTTATTGTCC AGAAGGAATC	240
AGTCAGCTAG AACCTCGTTC AGACTACGAC TATCTAGCCT TTATGCCAGT TCGGGATAGC	300
CAAGTATGAG TTGACAGAGG AAAATTTTTT CTTTAAAAAA GTGTACGCTT CTAACGAATA	360
TATAGATAGG GAACTGTCCG TAACTTGCCC AGATGGTTAT GTGGTCGTAC TGCA TAGCAA	420
GGACAGGAGG TAGGATGGAA AGTTTACTTA TTCTTATTATT AATTGCCAAT CTAGCTGGTC	480
TCTTTCTGAT TTGGCAAAGG CAGGATAGGC AGGAGAAACA CTTAAGTAAG AGCTTGAGG	540
ATCAGGCAGA TCATTTGTCA GACCAGCTGG ATTACCGCTT TGACCAAGCC AGACAAGCCA	600
GCCAGTTAGA CCAAAAAGAT TTGGAAGTGG TTGTCAAGCGA CCGTTTGCAA GAA	653

(2) INFORMATION FOR SEQ ID NO: 359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 641 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

CACCATGTGA TGTGACGCTG GCCACAGCTG TCAGAAATCT GGCGAGCCAT CGTGTGCAAT	60
GACTCTTCCC GATGTAATCT TGTTCATAGT CCTTTGATGA ATATGTTCAA GCTGTAGAAG	120
GTGCGCTTCC TGAACACTTA TCAACTGTTA CAGGGAGTT GACCAGTCAG GAAACAGATG	180
GCTGGTACAC ACTTGCCAAC ACTTCTTCAT CCCGCATTAA CCTAAACAA GCCTTCCAAG	240
AAAATAGCAA CCTCCTAGAG CAAGTGGTAG AACCCCTTGAC TATTATCACT GGTGGACACA	300
ACCAACAAGGA CCAGTTGACC TATGCTTGGAA AAACACTTTT GCAGAAATGCG CCACATGATA	360
GTATCTGTGG CTGTAGCGTG GACGAAGTTC ACCGGAGAT GGAAACCGT TTTGCCAAGG	420

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TCAACCAAGT AGGAAACTTT GTTAAAAGTA ACTTGCTCAA CGACTGGAAG GGTAAAATTG	480
CTACGGATAA GGCTCAAAGT GACTATCTCT TTACTGTCAT TAACACAGGC TTGCATGATA	540
AGGTGATAC TGTCAGCACA GTGATTGATG TGGCGACTTG TGATTTCAAG GAATTGCACC	600
CAACAGAAGG CTACAAAAG ATGGCTGCTC TTATCTTGCC G	641

(2) INFORMATION FOR SEQ ID NO: 360:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1958 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

CCTCAAGGCC AATTTGAAGG CTCTAAAACA ATGGAAAAGT GCTACACAGA TGTGACAGAA	60
TTTGCCATTC CAGCAAGTAC TCAAAAGCTT TACTTATCAC CAGTTTTAGA TGGCTTTAAT	120
AGCGAAATTA TTGCTTTAA TCTTTGACT TCACCCAACT TAGAACAGT ACAAAACAATG	180
TTAGAACAGG CATTCAAAGA GAAGCACTAC GAGAACATCGA TTCTCCATAG TGACCAAGGC	240
TGGCAATATC AACACGGATTC TTATCATCGG TTCCCTAGAGA GTAAGGGAAT TCAACCATCT	300
ATGTCACGCA AGGGCAACAG CCAAGACAAAC GGTATGATGG AATCTTTCTT TGGCATTTTA	360
AAATCCGAAA TGTTTTATGG CTATGAGAAA ACATTTAAAT CACTTAACCA ATTGGAACAA	420
GCCATTATAG ACTATATTGA TTACTACAAAC AACAAACGAA TTAAGGTAAA ACTAAAAGGA	480
CTTAGTCCTG TCCAGTACAG AACTAAATCC TTTGGATAAA TTAATTGTCT AACTTTTG	540
GGTCAGTACA AAACTCTTGC TACTATGCGT TTTATTATTG AAAGACTTAT TGGACTTTCT	600
CTCAAATCGA GTTTTTACTC AATTTCTTA CTTGATTGGG ATTGAAATTC CAATTAATT	660
CTCTGAGTAG AGTGTCTTGA TATTGGCTTC ATCAACAGAG GCCTTATCAA TTTTACGTT	720
CAAGAAAAAT TCTTGAATGG TTTCGATTTG AGGCTCACGA ATAGCACGGT GTTTGTGTTGA	780
GATGAGGATT TCATAGTGAA GCGGAGCTTG GGTAAAATA ACATCTGTAT TCCCTGCAGA	840
ATAAACCTCA ACAAGGGTTG CATCGGTACT TTCTAGCTGA CTTTTTACAA GTTGCAGTG	900
TGAGTTTGTGTC GTATTGATAA GCTTCATAAT ATTCCTCCG ATTTTCTAAT TCTATTATAG	960
CACTTTTGAA ATAAAGTCGC TTGATTATA CTCAAATGAAA ATCAAAGAGC AAACATAGGAA	1020
GCTAGCCGCA GCTATACATT GAGTACGGTA AGGCAGCGCT GACGTGGTTT GAATTTTATT	1080
TTCGAAGAGT ATTAGCCAAT CTTATGCTGT TTTTTCCAAG ATTCAATGGC CCATTTATGG	1140

1374	
CTACCACGTT TAAGGTTTT GATAGCCTCG TCAATAGGGA ACCAGGCAAT ATGATTAAAG	1200
TTTTCTAGTG GCTTTGTAC TTCTTGAAA GGAGTTGCTT CATAGAGGTA GGCAGGATTG	1260
TAGTAGTAGG TATCACGATG ACGAGAATAG AAATATTCGT CAGCTTGTCC GTAATAGGTA	1320
CCAATTCTG CTGTGAAACC AAGCTCTCA ATCAACTCAT GCTTTAGGGC TTCCTGATGA	1380
TTTTCACCTG CTTCAATTTC TCCACATGGT AGGAACCAAG CACCATTGGG TTCTTGAACA	1440
AGAACAAATTG TTTTTGTTC AGGATTAGGG ATAACATGCAT ATACGCCATA GCGAGCAATA	1500
TAGTCTGTAT TCACTTTTT TCTCCGAAAG TTGGGTTGC CATTGCATTTC TCCTCATTAT	1560
CTAGTATCGT TATTATTATA GTGAAATGAA CCAAAATAG TACACAATGT GGTATAATCT	1620
TCTTATGGCA TATTCAATAG ATTTTCGTAA AAAAGTTCTC TCTTATTGTG AGCGAACAGG	1680
TAGTATAACA GAAGCATCAC ACGTTTCCA AATCTCACGT AATACCATTG ATGGCTGGTT	1740
AAAGCTAAAA GAGAAAACAG GAGAGCTAAA CCACCAAGTA AAAGGAATAA AACCAAGAAA	1800
GGTTGATAGA GATAGACTTA AAAACTATCT TACTGACAAT CCAGACGCTT ATTTGACTGA	1860
AATAGCTTCT GAATTTGGCT GTCATCCAAC TACCATCCAC TATGCGCTCA AAGCTATGGG	1920
tACACTCGAA AAAAAAAAGA ACTACACCTA CTATGAAC	1958

(2) INFORMATION FOR SEQ ID NO: 361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 851 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

TATGAAATTA AGTTATGATG ATAAAGTTCA GATCTATGAA CTTAGAAAAC AAGGATATAG	60
CTTAGAGAAG CTTTCAAATA AATTTGGGAT AAGACAATTCT AATCTTAGGT ATATGATTAA	120
ATTGATTGAT CGTTACGGAA TAGAGTTCGT CAAAAAAAGGA AAAAATCGTT ACTATTCTCC	180
TGATTAAAAA CAAGAAATGA TTAATAAAAGT CTGACATGAA GGCTGGACTA AAGATAGAGT	240
TTCTCTGAA TACGGTCTCC CAAGTCGTAC GATACTTCTT AACTGGCTAG CACAATACAG	300
AAAAAACGGG TATACTATTG TTGAGAAACC AAGAGGGAGA GTACCTGAGA GCGGAGAATG	360
CCATCCTAAA AAAGTTAAGA GAACTCCGAT TGAAGGAGGA AAAAGAGAAA GAAGAAAGAC	420
AGAAATTGTT TAAGAATTAA TGACTGAGTT TTCGTTAGAT CTTCTTTAA AAGTCATTAA	480
ACTAGCTCGT TCGACCTACT ACTATCACTT GAAACAGCTA GATAAAACCAG ATAAGGACCA	540
AGAGCTTAAA GCTGAAATTC AATCCATTTC TATCGAACAC AAAGGAAATT ATGCTTATCG	600

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TCGGATTAT TTAGAACTAA GAAATCGTGG TTATCTGGTA AATCATAAAA GAGTTCAAGG	660
CTTGATGAAA GTACTCAATT TACAAGCTAA AACCGCAGAC AACGAAAAT ATTCTTCTCA	720
TAAAGGAGAC GTTGGCAAGA AGGCAGAGAA TCTCATTCAA GGCCAATTG AAGGCTCTAA	780
ACAAATGGAA CAGTGCTACA CAGATGTGAC AGAATTGCC ATTCCAGTAA GTACTAAAAA	840
GCTTTACTTA T	851

(2) INFORMATION FOR SEQ ID NO: 362:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1168 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

GGGTAGAACG GATATCTCCA ATGAGTTGGT TAGCTGGTG AAACTGTAAA AAGATTCGw	60
CCAATTCAAG GTTGAGGCAT CGCAAACAT GGACTGTTTC CTGGTCAGTT CTGGAAAGAA	120
AACGGGATAA GGTTGGCTGT GAAGCAAGCT GCCCTCCTTC CAACAATTGTT GGAAAGTAGG	180
CATCAGCTGA CAATTCTTTA CAAGCATAGT CCGTCCATA ACCTGTTAAC AGTTGAAAGA	240
GGAACTGGAC AAGGATATCT GAATCCGAAT AACGACAGTA GCGGCCTTGG TCATTCGTTA	300
CTAAATACTT AGAAATCCGC TCTTTAGTT TCAACTGGGA AAAAAGTTCC TGAAAAAAGA	360
TAAGACCACC ATACTGGTT AAATGACCTC CATCGAAAGA TAGTTGGTAA AAAGACTTGT	420
TTTGGAAAGTG ATGATTGGT AAACTGTTCA TGTGAGTTTC CTTCTTTTT GTGTTTTTT	480
CTACACTTAT ACCATAAAGG GGAAACTCTT TTTGTCTAG TAAAAAACAC CCATTGGGTG	540
AAAAAAGAAA CCATCCAGGA TCTAAGCTAA GGCAAGGATT CTGGATGGTT TTTAGATTTG	600
GGGTGAATAA TTGGGGTTTT AGCTGCTTGC GGCCAATCAG GTTCAGATAC AAAAACTTAC	660
TCATCAACCT TTAGTGGAAA TCCAACCTACA TTTAACTATC TATTAGACTA TTACGCTGAT	720
AATATAGTCA ATTGAAACAA GAACAAGACAA AAAGAGCCTC ATAAAAGGTA TTGCAACTTG	780
GTAATACCTT TTTGAGGTGC TTTTGATAT GAGCCCATGT TTTCTCAATA GGATTGTACT	840
CAGGTGAGTA GGGAGGAAGA GGTAAAAGTT TATAACCCAAA CTCTTCACAC AAGAGTTCTA	900
ACTTACCCAT TCTATGGAAT CTTGCATTAT CCATAATAAT AACCGATGGT GTGTTTAATG	960
TTGGTAAGAG AAATTTCTGA AACCAAGCTT CAAAAAGTC GCTCGTCATC GTCTCTCGT	1020
AAGTTATTGG AGCGATTAAC TCACCATTTG TTAGACCTGC AACCAAAGAA ATCCTCTGAT	1080

ATCTTCTTCC AGATACTTTG CCTCTTCTTA ACTGACCTTT TAATGAGCGA CCATATTCTC	1140
GATAAAAATA AGTATCGAAT CCTGTTTC	1168

(2) INFORMATION FOR SEQ ID NO: 363:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4483 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

GTCAGCTTCA GCAAGCCCAT CAGCTTCTGA ATCTGCATCA ACCAGTGCCTT CCGCTTCAGC	60
GTCAACCACTT GCGTCGGCTT CAGCGTCGAC AAGTGCCTTG GCTTCAGCAT CAACGAGTGC	120
GTCGGCCTCA GCAAGCGCAA GTACCTCAGC GTCAGCTTCC GCCTCAACCA GTGCGTCGGC	180
TTCAGCAAGC ACAAGTGCCTT CAGCCTCAGC AAGTATCTCA GCGTCTGAAT CGGCATCAAC	240
GAGTGCCTCT GAGTCAGCAT CAACGAGTAC GTCAGCTTCA GCAAGCACAT CAGCTTCTGA	300
ATCTGCATCA ACCAGTGCCTT CAGCCTCAGC ATCGACAAGC GCCTCAGCTT CAGCAAGTAC	360
CAGTGCTTCA GCCTCAGCGT CGACAAGTGC GTCGGCCTCA ACCAGTGCAT CTGAATCGGC	420
ATCAACCACTT GCGTCAGCCT CAGCAAGTAC TACTGCATCA GCTTCAGCAT CAACGAGTGC	480
ATCGGCTTCA GCATCAACCA GTGCCCTCGGC TTCAGCGTCA ACCAGTGCCTT CAGCTTCAGC	540
AAGTACCACTT GCTTCAGTCT CAGCATCAAC AAGTGCCTCA GCCTCAGCAT CGACAAGTGC	600
CTCGGCTTCA GCAAGCACAT CAGCATCTGA ATCAGCGTCG ACAAGCGCCT CAGCTTCAGC	660
AAGTACCACTT GCGTCAGCCT CAGCGTCGAC AAGTGCCTCA GCCTCAGCAA GTACTAGTGC	720
ATCAGCTTCA GCATCAACGA GTGCATCGGC TTCAGCGTCA ACCAGTGCAT CAGAGTCAGC	780
AAGTACCACTT GCGTCAGCCTT CCGCATCAAC AAGTGCCTCG GCTTCAGCAA GCACCAGTGC	840
GTCCGGCTTCA GCAAGTACTA GCGCCTCAGC CTCAGCTTCA ACCAGTGCCTT CAGCCTCAGC	900
AAGTATCTCA GCGTCTGAAT CGGCATCAAC GAGTGCCTCC GCTTCAGCAA GTACTAGCGC	960
CTCAGCTTCA GCGTCAACAA GTGCATCGGC TTCAGCGTCA ACCAGTGCCTT CTGAATCGGC	1020
ATCAACCACTT GCGTCCGCTT CAGCAAGTAC TAGCGCCTCA GCCTCAGCGT CAACAAAGTGC	1080
ATCGGCTTCA GCATCAACGA GTGCCTCGGC TTCAGCAAGT ACTAGCGCCT CAGCCTCAGC	1140
GTCAACCACTT GCGTCCGCTT CAGCGTCAC GAGTGCCTCT GAGTCAGCAT CAACGAGTGC	1200
GTCAGCTTCA GCAAGCACAT CAGCTTCTGA ATCTGCATCA ACCAGTGCCTT CAGCCTCAGC	1260
ATCGACAAGC GCCTCAGCTT CAGCAAGTAC CAGTGCCTCA GAGTCAGCGTC GACAAGTGCs	1320

1377

TCrGCTTCAG	CAAGTACCAAG	TGGTCAGCC	TCAGCAAGTA	CCAGTGCKTC	AGCCTCAGCG	1380
TCGACAAGTG	CGTCGGCCTC	AACCAGTGCA	TCTGAATCGG	CATCAACCAG	TGGTCAGCC	1440
TCAGCAAGTA	CTAGCGCCTC	AGCCTCAGCA	TCAACGAGTG	CGTCCGCTTC	AGCAAGTACT	1500
AGTGCATCAG	CTTCAGCAAG	TACTAGCGCC	TCAGCCTCAG	CGTCGACAAG	CGCCTCAGCT	1560
TCAGCAAGTA	CCAGTGCCTC	AGCCTCAGCG	TCGACAAGTG	CGTCCGCTTC	AGCAAGTACC	1620
TCAGCGTCTG	AATCAGCATH	AACAAGTGCG	TCGGCTTCAG	CATCAACGAG	TGCATCAGCT	1680
TCAGCATCAA	CAAGTGCTTC	AGCTTCAGCA	AGTACCAAGTG	CGTCCGCTTC	AGCATCAACG	1740
AGTGCCTCAG	TCTCAGCGTC	AACCAGTGCC	TCTGAATCCG	CATCAACAAG	TGCCTCGGCT	1800
TCAGCAAGCA	CCAGTGCTTC	GGCTTCAGCG	TCAACGAGTG	CGTCTGAGTC	AGCATCAACG	1860
AGTGCCTCAC	CTCAGCAAGC	ACATCAGCTT	CTGAATCTGC	ATCAACCAAGT	GCGTCACCTTC	1920
CGCATCAACA	AGGCCTCGG	CCTCAGCAAG	TACAAGTGCT	TCAGCCTCAG	CATCAACCAG	1980
TGCATCAGCT	TCAGCCTCAA	CAAGTGCTTC	AGCCTCAGCG	TCAACCAGTG	CCTCGGCTTC	2040
AGCAAGTACC	AGTGCCTCAC	CTTCAGCAAG	CACAAGTGCG	TCAGCCTCAG	CATCAACCAG	2100
TGCTTCGGCT	TCGGCATCAA	CAAGTGCCCTC	AGCAGTACCA	TCAACGAGTG	CGTCAsCTCA	2160
GCAAGTACTA	GTGCATCAGC	ATCAGCATCA	ACCAGTGCAT	CAGCCTCAGC	AAGTATCTCA	2220
GCGTCTGAAT	CGGCATCAAC	GAGTGCATCA	GCATCAGCAT	CAACGAGTG	ATCGGCTTC	2280
GCGTCAACCA	GTGCATCAGT	CTCAGCAAGC	ACCAGTGCCTG	CGGCTTCAGC	ATCAACCAAGT	2340
GCCTCAGCCT	CAGCAAGTAT	CTCAGCGTCT	GAATCGGCAT	CAACGAGTG	GTCAGCCTCA	2400
GCAAGTACTA	GTGCATCAGC	ATCAGCATCA	ACGAGTGCAT	CGGCTTCAGC	AAGTACCAAGC	2460
GCCTCAGCCT	CAGCAAGCAC	CAGTGCCTCA	GCCTCAGCAA	GTACCAGCG	CTCAGCCTCA	2520
GCAAGCACCA	GTGCCTCAGC	TTCAGCAAGT	ACCAGTGCCTG	CAGCCTCAGC	GTCGACAAGT	2580
GCGTCGGCTT	CAGCAAGTAC	CTCAGCGTCT	GAATCAGCAT	CAACGAGTG	ATCAGCTTC	2640
GCATCAACAA	GTGCTTCAGC	TTCAGCAAGT	ACCAGTGCCTG	CGGCTTCAGC	ATCAACCAAGT	2700
GCTTCAGCTCT	CAGCGTCAAC	CAGTGCCTCT	GAATCAGCAT	CAACAAGTG	CTCGGCTTC	2760
GCAAGCACCA	GTGCGTCGGC	TTCAGCAAGT	ACTAGTGCAT	CGGCTTCAGC	ATCGACAAGT	2820
GCGTCTGAAT	CGGCATCAAC	GAGTGCCTCG	GCTTCAGCAT	CAACGAGTG	GTCAGCCTCA	2880
GCAAGCACAT	CAGCTTCTGA	ATCTGCATCA	ACCAGTGCCTG	CGGCTTCAGC	GTCAACCAAGT	2940
GCGTCGGCTT	CAGCGTGCAC	AAAGTGCCTCG	GCTTCAGCAT	CAACGAGTG	GTCGGCCTCA	3000
GCAAGCACAA	GTACCTCAGC	GTCAGCTTCC	GCCTCAACCA	GTGCGTCGGC	TTCAGCAAGC	3060

1378	
ACAAGTCCGT CAGCCTCAGC AAGTATCTCA GCGTCTGAAT CGGCATCAAC GAGTCCGTCG	3120
GCCTCAGCAA GCGCAAGTAC CTCAGCGTCA GCTTCGGCCT CAACCAAGTGC GTCGGCTTCA	3180
GCAAGCACAA GTCCGTCAGC CTCAGCAAGT ATCTCAGCGT CTGAATCGGC ATCAACGAGT	3240
GCGTCTGAGT CAGCATCAAC GAGTACGTCA GCCTCAGCAA GCACATCAGC TTCTGAATCG	3300
GCATCAACCA GTCCGTCAGC CTCAGCATCG ACAAGGCCT CAGCTTCAGC AAGTACCAAGT	3360
GCTTCAGCCT CAGCCTCGAC AAGTCCGTCG GCCTCAACCA GTGCATCTGA ATCGGCATCA	3420
ACCAGTCCGT CAGCCTCAGC AAGTACTAGT GCATCAGCTT CAGCATCAAC GAGTGCATCG	3480
GCTTCAGCAT CAACCAAGTGC CTCGGCTTCA GCGTCAACCA GTCCGTCAGC TTCAGCAAGT	3540
ACCAGTGCCTT CAGTCTCAGC ATCAACAAAGT GCTTCAGCCT CAGCATCGAC AAGTCCGTCG	3600
GCTTCAGCAA GCACATCAGC ATCTGAATCA GCGTCGACAA GCGCCTCAGC TTCAGCAAGT	3660
ACCAGTCCGT CAGCCTCAGC GTCGACAAAGT GCGTCAGCCT CAGCAAGTAC TAGTGCATCA	3720
GCTTCAGCAT CAACGAGTGC ATCGGCTTCG GCGTCAACCA GTGCATCAGA GTCAGCAAGT	3780
ACCAGTCCGT CAGCTCCGC ATCAACAAAGT GCCTCGGCTT CAGCAAGCAC CAGTCCGTCG	3840
GCTTCAGCAA GTACTAGCGC CTCAGCCTCA GCCTCAACCA GTCCGTCAGC CTCAGCAAGT	3900
ATCTCAGCGT CTGAATCGGC ATCAACAGGT GCGTCCGCTT CAGCAAGTAC TAGGCGCTCA	3960
GCCTCAGCGT CAACAAAGTGC ATCGGCTTCA GCGTCAACGA GTCCGTCAGC ATCGGCATCA	4020
ACGAGTCCGT CCGCTTCAGC AAGTACTAGC GCCTCAGCCT CAGCGTCACAC AAGTGCATCG	4080
GCTTCAGCAT CAACGAGTGC GTCCGCTTCA GCAAGTACTA GCGCCTCAGC CTCAGCGTC	4140
ACAAGTGCAT CCGGTTTCAGC GTCAACAGGT GCGTCTGAGT CAGCATCAAC GAGTCCGTC	4200
CCTCAKCAAG CACATCAGCT TCTGAATCTG CATCAACCAAG TGCGTCACTT CCGCATCAAC	4260
AAGCGCCTCG GCCTCAGCAA GTACAAGTGC TTCAGCCTCA GCATCAACCA GTGCATCAGC	4320
TTCAAGTGCCT CAGCCTCAGC GTCAGACCAAG TGCGCTCGGCT TCAGCAAGTA	4380
CCAGTCCGTC ACTTCAGCAA GCACAAGTGC GTCAGCCTCA GCATCAACCA GTGCTTCGGC	4440
TTCCGGCATCA ACAAGTGCCT CAGCATCAGC ATCAACAGGT GCG	4483

(2) INFORMATION FOR SEQ ID NO: 364:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2550 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

1379

GTACCTCAGC	GTCCCTCCGC	CTCAACCAGT	GCGCCGCTT	CAGCAAGCAC	AAGTGCGTCA	60
CCTCAGCAAG	TATCTCAGCG	TCTGAATCGG	CATCAACGAG	TGGCTCGGCC	TCAGCAAGCG	120
CAAGTACCTC	AGCGTCACTT	CCGCCTCAAC	CAGTGCCTCG	GCTTCAGCAA	GCACAAGTGC	180
GTCAsCTCAG	CAAGTATCTC	AGCGTCTGAA	TCGGCATCAA	CGAGTGCCTC	TGAGTCAGCA	240
TCAACGAGTA	CGTCAGCCTC	AGCAAGCAC	TCAGCTCTG	AATCGGCATC	AACCAACTGCG	300
TCAGCCTCAG	CATCGACAAG	CGCCTCAGCT	TCAGCAAGTA	CCAGTGCCTC	AGCCTCAGCG	360
TCGACAAGTG	CGTCGGCCTC	AACCAGTGCA	TCTGAATCGG	CATCAACCAG	TGGCTCAGCC	420
TCAGCAAGTA	CTAGTCATC	AGCTTCAGCA	TCAAACGAGTG	CATCGGCCTC	AGCATCAACC	480
AGTGCCCTCGG	CTTCAGCGTC	AACCAGTGC	TCAGCTTCAG	CAAGTACCGAG	TGCTTCAGTC	540
TCAGCATCAA	CAAGTGCTTC	AGCCTCAGCA	TCGACAAGTG	CCTCGGCTTC	AGCAAGCACA	600
TCAGCATCTG	AATCAGCGTC	GACAAGTGC	TCGGCCTCAA	CCAGTGCATC	TGAATCGGCA	660
TCAACCAGTG	CGTCAGCCTC	AGCAAGTACT	AGTCATCAG	CTTCAGCATC	AACGAGTGCA	720
TCGGCTTCGG	CGTCAACCAG	TGCATCAGAG	TCAGCAAGTA	CCAGTGCCTC	AGCTTCCGCA	780
TCAACAAGTG	CTCTGGCTTC	AGCAAGCACA	TCAGCATCTG	AATCAGCGTC	AACCAAGTGCT	840
TCGGCTTCAG	CAAGTACCGAG	TGCTTCAGCT	TCAGCATCAA	CCAGCCTCCTC	GGCCTCAGCA	900
AGCACCTCAG	CTTCTGAATC	GGCCTCAACC	AGGCCTCAGG	CCTCAGCAAG	CACCTCAGCT	960
TCTGAATCGG	CCTCAACCAG	CGCCTCAGCC	TCAGCATCAA	CGAGTGCCTC	GGCTTCAGCA	1020
AGCACAAAGCG	CCTCAGGTTTC	AGCATCAACG	AGTACGTCAG	CTTCAGCGTC	AACCAAGTGCT	1080
TCAGCCTCAG	CATCAACAAG	TGCCAGGCC	TCAGCAAGTA	TCTCAGCGTC	TGAATCGGCA	1140
TCAACGAGTG	CGTCTGAGTC	AGCATCAACG	AGTACGTCAG	CCTCAGCAAG	CACAAGTGCT	1200
TCAGCCTCAG	CAAGTATCTC	AGCGTCTGAA	TCGGCATCAA	CGAGTGCCTC	CGCTTCAGCA	1260
AGTACTAGCG	CCTCAGCATC	AGCGTCAACA	AGTGCTTCGG	CTTCAGCGTC	AACGAGTGCG	1320
TCTGAGTCAG	CATCAACGAG	TACGTCAAGCC	TCAGCAAGCA	CATCAGCTTC	TGAATCTGCA	1380
TCAACCAGTG	CGTCAGCCTC	AGCATCGACA	AGGCCTCAG	CTTCAGCAAG	TACCAAGTGC	1440
TCAGCCTCAG	CAAGTACCGAG	TGCTTCAGCC	TCAGCGTCGA	CAAGTGCCTC	GGCCTCAACC	1500
AGTGCATCTG	AATCGGCATC	AACCAGTGCG	TCAGCTCAGC	AAGTACTAGT	GCATCAGCTT	1560
CAGCATCAAC	GAGTGCATCG	GCTTCGGCGT	CAACCAAGTGC	ATCAGAGTCA	GCAAGTACCA	1620
GTGCGTCACT	TCCGCATCAA	CAAGTGCCTC	GGCTTCAGCA	AGCACATCAG	CATCTGAATC	1680
AGCGTCAACC	AGTGCTTCGG	CTTCAGCAAG	TACCAAGTGC	TCAGCTTCAG	CATCAACCAG	1740

1380						
CGCCTCGGCC	TCAGCAAGCA	CCTCAGCTTC	TGAATCGGCC	TCAACCAGCG	CCTCGGCCTC	1800
AGCAAGCACC	TCAGCTTCTG	AATCGGCCTC	AACCAGCGCC	TCAGCCTCAG	CATCAACGAG	1860
TGCTTCGGCT	TCAGCAAGCA	CAAGCGCCTC	GGGTTAGCA	TCAACGAGTA	CGTCAGCTTC	1920
AGCGTCAACC	AGTGCTTCAG	CCTCAGCATC	AACAAGTGC	TCAGCCTCAG	CAAGTATCTC	1980
AGCGTCTGAA	TCGGCATCAA	CGAGTGCAGTC	TGAGTCAGCA	TCAACGAGTA	CGTCAGCCTC	2040
AGCAAGCACC	TCAGCTTCTG	AATCGGCCTC	AACCAGTGC	TCAGCCTCAG	CATCGACAAAG	2100
CGCCTCAGCT	TCAGCAAGTA	CCAGTGCTTC	AGCCTCAGCG	TGACAAAGTG	CGTCGGCCTC	2160
AACCAGTGCA	TCTGAATCGG	CATCAACCAG	TGCGTCAGCC	TCAGCAAGTA	CTAGTGCATC	2220
GGCTTCAGCA	TCAACCAAGTG	CCTCGGCCTC	AGCGTCAACC	AGTGCAGTCAG	CTTCAGCAAG	2280
TACCAAGTGCT	TCAGTCTCAG	CATCAACAAAG	TGCTTCAGCC	TCAGCATCGA	CAAGTGCCTC	2340
GGCTTCAGCA	AGCACATCAG	CATCTGAATC	AGCGTCAGCA	AGCGCCTCAG	CTTCAGCAAG	2400
TACCAAGTGCG	TCAGCCTCAG	CGTCAGCAAG	TGCGTCAGCT	ACAGCAAGTA	CTAGTGCATC	2460
AGCTTCAGCA	TCAACGAGTG	CATCGGCCTC	GGCGTCAACC	AGTGCATCAG	AGTCAGCAAG	2520
TACCAAGTGCG	TCAGTTACAG	CATCAACAAAG				2550

(2) INFORMATION FOR SEQ ID NO: 365:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1436 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

ACCCAGCAAG	TACTAGTGCA	TCGGCTTCAG	CAAGCACCAG	TGCGTCGGCT	TCAGCATCAA	60
CCAGTGCCTC	AGCCTCAGCA	AGTATCTCAG	CCTCTGAATC	GGCATCAACG	AGTGCAGTCAC	120
CTCAGCAAGT	ACTAGTGCAT	CAGCATCAGC	ATCAACGAGT	GCATCGGCTT	CAGCAAGTAC	180
CAGCGCCTCA	GCTTCAGCAA	GCACCAAGTGC	GTCAsCTCAG	CAAGTACCAAG	CGCCTCAGCC	240
TCAGCAAGCA	CCAGTGCCTC	AGCTTCAGCA	AGTACCAAGT	CGTCAGCCTC	AGCGTCAGCA	300
AGTGCAGTCGG	CTTCAGCAAG	TACCTCAGCG	TCTGAATCAG	CATCAACGAG	TGCACTCAGCT	360
TCAGCATCAA	CAAGTGCCTC	AGCTTCAGCA	AGTATCTCAG	CCTCTGAATC	GGCATCAACG	420
AGTGCAGTCGG	CTTCAGCAAG	TACTAGCGCC	TCAGCATCAG	CGTCAGCAGCA	TGCTTCGGCT	480
TCAGCGTCAA	CGAGTGCAGTC	TGAGTCAGCA	TCAACGAGTA	CGTCAGCCTC	AGCAAGCACA	540
TCAGCTTCTG	AATCTGCATC	AACCAGTGC	TCAGCCTCAG	CATCGACAAAG	CGCCTCAGCT	600

1381

TCAGCAAGTA CCAGTGCCTC AGCCTCAGCA AGTACCAAGTG CTTCAGCCTC AGCGTCGACA	660
AGTGCCTCGG CCTCAACCG TGCATCTGAA TCGGCATCAA CCAGTGCCTC AGCCTCAGCA	720
AGTACTAGCG CCTCAGCCTC AGCATCAACG AGTGCCTCGG CTTCAGCAAG TACTAGTGCA	780
TCAGCTTCAG CAAGTACTAG CGCCTCAGCC TCAGCGTCGA CAAGCGCCTC AGCTTCAGCA	840
AGTACCAAGTG CGTCAGCCTC AGCGTCGACA AGTGCCTCGG CTTCAGCAAG TACCTCAGCG	900
TCTGAATCAG CATCAACAAAG TGCGCTGGCT TCAGCATCAA CGAGTGCATC AGCTTCAGCA	960
TCAACAAGTG CTTCAGCCTC AGCAAGTACC AGTGCCTCGG CTTCAGCATC AACGAGTGCT	1020
TCAGTCTCAG CGTCACCCAG TGCCCTCTGAA TCCGCATCAA CAAGTGCCTC GGCTTCAGCA	1080
AGCACCAAGTG CTTCGGCTTC AGCGTCAACG AGTGCCTCTG AGTCAGCATC AACGAGTGCG	1140
TCAGCCTCAG CAAGCACATC AGCTTCAGGAA TCTGCATCAA CCAGTGCCTC AGCTTCAGCA	1200
TCAACAAGCG CCTCGGCCTC AGCAAGTACA AGTGCCTCAG CCTCAGCATC AACCAAGTGCA	1260
TCAGCTTCAG CCTCAACAAAG TGCTTCAGCC TCAGCGTCAA CCAGTGCCTC GGCTTCAGCA	1320
AGTACCAAGTG CGTCAGCCTC AGCAAGCACA AGTGCCTCAG CTTCAGCATC AACCAAGTGCT	1380
TCGGCTTCGG CATCAACAAAG TGCCCTCAGCA TCAGCATCAA CGAGTGCCTC AGCCGG	1436

(2) INFORMATION FOR SEQ ID NO: 366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 735 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

GCAGTTGCCA CACCGTCTG ACCAGCACCC GTTCTGCCA TAATTTCTT TTTACCCATG	60
CGTWTGGCAA GCCAAACTTG TCCTAAGGCA TTGTTAATCT TGTGGGCTCC TGTATGGTTA	120
AGGTCTTCCC GTTTGAGATA AATCTTGCTC CGCCAATATG CTGGGTCAAG TTTTTTGCCT	180
AATAAAAGAGG AGTTTACGT CCTACGTACT GGCAGAAAG CTGGTTAAT TCCTCTGGAA	240
AACTTGGTC TGCTGACTT TCACGGTAGG CCTCTCCAA CTCCAAACT GCTGTCATCA	300
ATGTTTCTGG GACAAAACGT CGGGGAATT TTCCGTTAAAC TCCATTTTA TTTGGTTCCCT	360
GATATGCCAT GCTTTPACCT CTCTATAAAAT CTTCTAATCT TTTCATGATC TTTTTGTCCA	420
TCTGTCTCCA CTCCGCTCGA TACATCTACT GCATAGGGAG TAAAGTGTG AATTGCTTTT	480
ACTACATTAT CTTCATTAAG GCCACCTGCG ATAAAGAAGG CCTGTGCTAG TCCAGTCGTA	540

1382	
TCCAGTGAC CCCAATCAA GGGCTGGCCA CTTCCCTGCCA CAGGGGCATC AAAGAGTAGA	600
TAATCTGCCCT GAGAAATTGGG GACATGCCCA TTTCCATCTA CCTGCACAGC CTGAATACTG	660
GCACAAGGCA AATTCTCAA TAAATCATCT GCCACCTGAC CGTGAACATTG AACCAAGTCC	720
AAGCCGGGGA TCCTC	735

(2) INFORMATION FOR SEQ ID NO: 367:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1702 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

TACTAGCGCC TCAGCCTCAG CGTCAACAAG TGCATCGGCT TCAGCATCAA CGAGTGCCTC	60
CGCTTCAGCA AGTACTAGCG CCTCAGCCTC AGCGTCAACA AGTGCATCGG CTTCAGCGTC	120
AACGAGTGCG TCTGAGTCAG CATCAACGAG TGCAGTCAGCC TCAGCAAGCA CATCAGCTTC	180
TGAATCTGCA TCAACCAAGTG CGTCAGCCTC AGCATCGACA AGCGCCTCAG CTTCAGCAAG	240
TACCAGTGCG TCAGCCTCAG CGTCAGACAAG TGCAGTCGGCT TCAGCAAGTA CCAGTGCCTC	300
AGCCTCAGCA AGTACCAAGTG CGTCAGCCTC AGCGTCGACA AGTGCAGTCGG CCTCAACCAG	360
TGCATCTGAA TCGGCATCAA CCAGTGCCTC AGCCTCAGCA AGTACTAGTG CATCAGCTTC	420
AGCATCAACG AGTGCATCGG CTTCAGCCTC AACCAGTGCA TCAGAGTCAG CAAGTACCAAG	480
TGCAGTCAGCT TCCGCATCAA CAAGTGCCTC GGCTTCAGCA AGTACTAGCG CCTCAGCCTC	540
AGCGTCAACA AGTGCTTCAG CTTCCCGCTC AACCAGCGCC TCGGCCTCAG CAAGTATCTC	600
AGCGTCTGAA TCGGCATCAA CAAGTGCCTC GGCTTCAGCA TCAACAGAGTG CATCAGCTTC	660
AGCAAGCACC AGTGCCTCAG CCTCAGCAAG CACCAGCGGG TCTGAATCCG CATCAACCAG	720
TGCCTCAGCT TCAGCAAGTA CCTCAGCCTC TGAATCAGCA TCAACAAAGTG CATCGCTTC	780
AGCAAGCACA AGTGCTTCAG CCTCAGCAAG TATCTCAGCG TCTGAATCCG CATCAACGAG	840
TGCCTCAGCT TCAGCAAGTA CTAGCCTCAG CCTCAGCAAG TCAACAAAGTG CTTCAGCTTC	900
AGCGTCAACG AGTGCCTCAG AGTCAGCCTC AACAGAGTGAG TCAGCCTCAG CAAGCACATC	960
AGCTTCTGAA TCTGCATCAA CCAGTGCCTC AGCCTCAGCA TCGACAAAGCG CCTCAGCTTC	1020
AGCAAGTACG AGTGCCTCAG CCTCAGCAAG TACCAAGTGCT TCAGCCTCAG CGTCGACAAG	1080
TGCCTCAGGCC TCAACCAAGTG CATCTGAATC GGCATCAACC AGTGCCTCAG CCTCAGCAAG	1140
TACTAGCGCC TCAGCCTCAG CATCAACGAG TGCAGTCGGCT TCAGCAAGTA CTAGTGCATC	1200

1383

AGCATCAGCA TCAACGAGTG CATCGGCTTC AGCAAGTACC AGCGCCTCAG CTTCAGCAAG	1260
CACCAAGTGCG TCAGCCTCAG CAAGTACAG CGCCTCAGCC TCAGCAAGCA CCAGTGCTC	1320
AGCTTCAGCA AGTACCAAGTG CGTCAGCCTC AGCGTCGACA AGTGCCTCGG CTTCAGCAAG	1380
TACCTCAGCG TCTGAATCAG CATCAACGAG TGCAATCAGCT TCAGCATCAA CAAGTGCTC	1440
AGCTTCAGCA AGTACCAAGTG CGTCGGCTTC AGCATCAACG AGTGCCTCAG TCTCAGCGTC	1500
AACCAAGTGCC TCTGAATCAG CATCAACAAAG TGCGTCGGCT TCAGCAAGCA CCAGTGCGTC	1560
GGCTTCAGCA AGTACTAGTG CATCGGCTTC AGCATCGACA AGTGCCTCGT AATCGGCATC	1620
AACGACTGCT TCGGCTCAG CATCAACGAG TGCGTCAGCC TCAGCAAGCA CATCAGCTTC	1680
TGAATCTGCA TCAACCAAGTG CG	1702

(2) INFORMATION FOR SEQ ID NO: 368:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 941 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

ACCAGTGCAT CAGCTTCAGC CTCAACAAAGT GCTTCAGCCT CAGCGTCAC CAGTGCCTCG	60
GCTTCAGCAA GTACCAGTGC GTCACTTCAG CAAGCACAAG TGCGTCACCT CAGCATCAAC	120
CAGTGCTTCG GCTTCGGCAT CAACAAAGTGC CTCAGCATCA GCATCAACGA GTGCGTACCC	180
TCAGCAAGTA CTAGTGCATC AGCATCAGCA TCAACCAAGTG CATCAGCCTC AGCAAGTATC	240
TCAGCGTCTG AATCGGCATC AACGAGTGCA TCAGCATCAG CATCAACGAG TGCGATCGGCT	300
TCAGCGTCAA CCAGTGCATC AGTCTCAGCA AGCACCAAGTG CGTCGGCTTC AGCATCAACG	360
AGTGCCTCAG CCTCAGCAAG TATCTCAGCG TCTGAATCGG CATCAACGAG TGCGTCAGCC	420
TCAGCAAGTA CTAGTGCATC GGCTTCAGCA AGCACCAAGTG CGTCGGCTTC AGCATCAACC	480
AGTGCCTCAG CCTCAGCAAG TATCTCAGCG TCTGAATCGG CATCAACGAG TGCGTCAGCC	540
TCAGCAAGTA CTAGTGCATC AGCATCAGCA TCAACGAGTG CATCGGCTTC AGCAAGTACC	600
AGCGCCTCAG CTTCAGCAAG CACCAAGTGGG TCAGCCTCAG CAAGTACCGAG CGCCTCAGCC	660
TCAGCAAGCA CCAGTGCTC AGCTTCAGCA AGTACCAAGTG CGTCAGCCTC AGCGTCGACA	720
AGTGCCTCGG CTTCAGCAAG TACCTCAGCG TCTGAATCAG CATCAACGAG TGCAATCAGCT	780
TCAGCATCAA CAAGTGCTTC AGCTTCAGCA AGTACCAAGTG CGTCGGCTTC AGCATCAACG	840

1384	
AGTGCTTCAG TCTCAGCGTC AACCAAGTGC C TCTGAATCAG CATCAACAAG TGCCTCGGCT	900
TCAGCAAGCA CCAGTGCAGTC GGCTTCAGCA AGTACTAGTG C	941

(2) INFORMATION FOR SEQ ID NO: 369:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 869 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

CAGCAAGTAC TAGTGCATCA GCTTCAGCAT CAACGAGTGC ATCGGCTTCT GCGTCAACCA	60
GTGCATCAGA GTCAGCAAGT ACCAGTGCCT CAGCTTCCCG ATCAACAAGT GCCTCGGCTT	120
CAGCAAGCAC CAGTGCCTCG GCTTCAGCAA GTACTAGCGC CTCAGCCTCA GCCTCAACCA	180
GTGCGTCAGC CTCAGCAAGT ATCTCAGCGT CTGAATCGGC ATCAACGAGT GCGTCCGCTT	240
CAGCAAGTAC TAGCGCCTCA GCCTCAGCGT CAACAAGTGC ATCGGCTTCA GCGTCAACGA	300
GTGCGTCTGA ATCGGCATCA ACGAGTGCCT CGCCTTCAGC AAGTACTAGC GCCTCAGCCT	360
CAGCGTCAAC AAGTGCATCG GCTTCAGCAT CAACGAGTGC GTCCGCTTCA GCAAGTACTA	420
GCGCCTCAGC CTCAGCGTCA ACAAGTGCAT CGGCTTCAGC GTCAACGAGT GCGTCTGAGT	480
CAGCATCAAC GAGTGCCTCA GCCTCAGCAA GCACATCAGC TTCTGAATCT GCATCAACCA	540
GTGCGTCAGC CTCAGCATCG ACAAGCGCCT CAGCTTCAGC AAGTACCAAGT GCGTCAGCCT	600
CAGCGTCGAC AAGTGCCTCG GCTTCAGCAA GTACCAAGTGC GTCAGCCTCA GCAAGTACCA	660
GTGCGTCAGC CTCAGCGTCA ACAAGTGCCT CGGCCTCAAC CAGTGCATCT GAATCGGCAT	720
CAACCAAGTGC GTCAGCCTCA GCAAGTACTA GTGCATCAGC TTCAGCATCA ACGAGTGCAT	780
CGGCTTCAGC ATCAACCAGT GCATCAGAGT CAGCAAGTAC CAGTGCCTCA GAGTGCCTCA	840
GCAACAAGTG CCTCGGCTTC AGCAAGTAC	869

(2) INFORMATION FOR SEQ ID NO: 370:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 750 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

TCAACAAAGTG CCTCAGCATC AGCATCAACG AGTGCCTCG C CTCAAGTGC TACTAGTGCA	60
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1385

TCAGCATCAG CATCAACCAAG TGCATCAGCC TCAGCAAGTA TCTCAGCGTC TGAATCGGCA	120
TCAACGAGTG CATCAGCATC AGCATCAACG AGTCATCGG CTTCAGCGTC AACCAAGTGCA	180
TCAGTCTCAG CAAGCACCAG TGCGTCGGCT TCAGCATCAA CGAGTGCCTC AGCCTCAGCA	240
AGTATCTCAG CGTCTGAATC GGCACTCAACG AGTGCAGTCAG CCTCAGCAAG TACTAGTGCA	300
TCGGCTTCAG CAAGCACCAG TGCGTCGGCT TCAGCATCAA CCAGTGCCTC AGCCTCAGCA	360
AGTATCTCAG CGTCTGAATC GGCACTCAACG AGTGCAGTCAG CCTCAGCAAG TACTAGTGCA	420
TCAGCATCAG CATCAACGAG TGCATCGGCT TCAGCAAGTA CCAGCGCCTC AGCTTCAGCA	480
AGCACCAAGTG CGTCAGCCTC AGCAAGTACG AGCCGCCTCAG CCTCAGCAAG CACCAAGTGCC	540
TCAGCTTCAG CAAGTACCAAG TGCGTCAGCC TCAGCGTCGA CAAGTGCAGTC GGCTTCAGCA	600
AGTACCTCAG CGTCTGAATC AGCATCAACG AGTCATCGAG CCTCAGCATC ACAAAAGTGCT	660
TCAGCTTCAG CAAGTATCTC AGCGTCTGAA TCGGCATCAA CGAGTGCAGTC CGCTTCAGCA	720
AGTACTAGCG CCTCAGCATC AGCGTCAACG	750

(2) INFORMATION FOR SEQ ID NO: 371:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 957 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

CCGGAAAACA GCTCTGGCGC TTGGTCTTGC CCAGCGTATT GCTAGTGGTG ACGTGCGCTGC	60
GGAAATGGCT AAGATGCGCG TGTAGAAACT TGATTTGATG AATGTCGTTG CAGGGACACG	120
CTTCCGTGGT GACTTTGAAG AACGCATGAA TAATATCATC AAGGATATTG AAGAAGATGG	180
CCAAGTCATC CTCTTTATCG ATGAACTCCA CACCATCATG GGTTCTGGTA CGGGGATTGA	240
TTCGACTCTG GATGCGGCCA ATATCTTGAA ACCAGCCTTG CGCGGTGGAA CTTTGAGAAC	300
GGTTGGTGCC ACTACTCAGG AAGAATATCA AAAACATATC GAAAAAGATG CGGCACTTTC	360
TCGTCGTTTC GCTAAAGTGA CGATTGAAGA ACCAAGTGTG GCAGATAGTA TGACTATTTT	420
ACAAGGTTTG AAGGGCAGTT ATGAGAAACA TCACCGTGTAA CAAATCACAG ATGAAGCGGT	480
TGAAACAGCG GTTAAGATGG CTCATCGTTA TTTAACAGT CGTCACTTGC CAGACTCTGC	540
TATCGATCTC TTGGATGAGG CGGCAGCAAC AGTGCAAAT AAGGCAAAGC ATGAAAAGC	600
AGACGATTCA GATTGAGTC CAGCTGACAA GGCCTGATG GATGGCAAGT GGAAACAGGC	660

AGCCCAGCTA ATCGAAAAG AAGAGGAAGT ACCTGTCTAC AAAGACTTGG TGACAGAGTC	1386 720
TGATATTTTG ACCACCTTGA GTCGTTGTC AGGAATCCCA GTTCAAAAAC TGACTCAAAC	780
GGATGCTAAG AAGTATTAA ATCTTGAAAGC AGAACTCCAT AAACGGGTTA TCGGTCAAGA	840
TCAAGCTGTT TCAAGCATTA GCCGTGCCAT TCGCCGCAAC CAGTCAGGGGA TTCCGAGTCA	900
TAAGGCTCCG ATTGGTCCCT TTATGTTCCCT AGGGCCTACA GGTGTCGGGG TATCCGA	957

(2) INFORMATION FOR SEQ ID NO: 372:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 807 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

CAAAGGCCCT CAGCTTCAGC ATCAACAAAGT GCGTCGGCTT CAGCATCAAC CAGTCGCTCG	60
GCTTCAGCGT CAACCAAGTGC GTCACATTCA GCAAGTACCA GTGCTTCAGT CTCAGCATCA	120
ACAAGTGCTT CAGCCTCAGC ATCGACAAGT GCCTCGGCTT CAGCAAGCAC ATCAGCATCT	180
GAATCAGCGT CAACCAAGTGC TTCCGCTTCA GCAAGTACCA GTGCTTCAGC TTCAGCATCA	240
ACCAAGGCCCT CGGUCUTCAAGC AAGCACCTCA GCTTCTGAAT CGGUCUTCAAC CAGCGGUCUTCG	300
GCCTCAGCAA GCACCTCAGC TTCTGAATCG GCCTCAACCA GCGCCTCAGC CTCAGCATCA	360
ACGAGTGCTT CGGCTTCAGC AAGCACAAGC GCCTCGGTT CAGCATCAAC GAGTACGTCA	420
GCTTCAGCGT CAACCAAGTGC TTCAACGAGT GCGTCTGAGT CAGCATCAAC GAGTACGTCA	480
ATCTCAGCGT CTGAATCGGC ATCAACGAGT GCGTCTGAGT CAGCATCAAC GAGTACGTCA	540
GCCTCAGCAA GCACCTCAGC TTCTGAATCG GCCTCAACCA GTGCGTCAGC CTCAGCATCG	600
ACAAGGCCCT CAGCTTCAGC AAGTACCAAGT GCCTCAGCCT CAGCGTCGAC AAGTGCCTCG	660
GCCTCAACCA GTGCATCTGA ATCGGCATCA ACCAGTGCAGT CAGCCTCAGC AAGTACTAGT	720
GCATCGGCTT CAGCATCAAC CAGTGCCTCG GCCTCAGCGT CAACCAAGTGC GTCAGCTTC	780
GCAAGTACCA TGTGCTTCAT GTCTCAG	807

(2) INFORMATION FOR SEQ ID NO: 373:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1068 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

1387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

CATCGGCTTC AGCATCAACG AGTGGTCCG CTTAGCAAG TACTACGCC TCAGCCTCAG	60
CGTCAACAAG TGCATCGCT TCAGCGCAA CGAGTGCCTC TGAGTCAGCA TCAACGAGTG	120
CGTCACCTCA GCAAGCACAT CAGCTTCTGA ATCTGCATCA ACCAGTGCCTC CACCTCAGCA	180
TCGACAAGCG CCTCAGCTTC AGCAAGTACC AGTGCCTCAC CTCAGCGCTC ACAAGTGCCTC	240
CGGCTTCAGC AAGTACCGAT GCGTCAsCTC AGCAAGTACC AGTGCCTCAC CTCAGCGCTC	300
ACAAGTGCCTC CGGCCTCAAC CAGTGCATCT GAATCGGCAT CAACCAGTGC GTCACCTCAG	360
CAAGTACTAG TGCATCAGCT TCAGCATCAA CGAGTGCATC GGCTTCAGCA TCAACCAGTG	420
CATCAGAGTC AGCAAGTACC AGTGCCTCAG CCTTCGGCATC ACAAGTGCCTC TCGGCTTCAG	480
CAAGTACTAG CGCCTCAGCC TCAGCGCTAA CAAAGTGCCTC AGCTTCGCG TCAACCAGCG	540
CCTCGGCTC AGCAAGTATC TCAGCGTCTG AATCGGCATC ACAAGTGCCTC TCGGCTTCAG	600
CATCAACGAG TGCATCAGTC TCAGCAAGCA CCAGTGCCTC GGCTTCAGCA AGCACCAGCG	660
CGTCTGAATC CGCATCAACC AGTGCCTCAG CCTTCAGCAAG TACCTCAGCA TCTGAATCAG	720
CATCAACAAG TGCATCGCT TCACCAAGCA CAAAGTGCCTC AGCCTCAGCA AGTATCTCAG	780
CGTCTGAATC GGCATCAACG AGTGCCTCAG CCTTCAGCAAG TACTAGCGCC TCAGCATCAG	840
CGTCAACAAG TGCTTCGGCT TCAGCGCTAA CGAGTGCCTC TGAGTCAGCA TCAACGAGTA	900
CGTCAGGCTC AGCAAGCACA TCAGCTTCTG AATCTGCATC ACCAGTGCCTC TCGGCTTCAG	960
CATCGACAAG CGCCTCAGCT TCAGCAAGTA CCAGTGCCTC AGCCTCAGCA AGTACCAAGTG	1020
CTTCAGGCTC AGCGTCGACA AGTGCCTCAG GCTCAACCAG TGCATCTG	1068

(2) INFORMATION FOR SEQ ID NO: 374:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

CAGCATCAAC GAGTGCCTCA GTTCAGCGT CAACCAAGTGC CTCTGAATCA GCTTCACAA	60
GTGCCTCGGC TTCAAGCAAGC CCCAGTGCCTC CGGCTTCAGC AAGTACTAGT GCATCGGCTT	120
CAGCATCGAC AAGTGCCTCT GAATCGGCAT CAACGAGTGC TTGGCTTCAGCA GCATCAACGA	180
GTGCCTCAGC CTCAGCAAGC ACATCAGCTT CTGAATCTGC ATCAACCAGT GCGTCCGyTT	240

1388	
CAGCGTCAAC CAGTGCCTCG GCTTCAGCGT CGACAAGTGC TTCCGGCTTCA GCATCAACGA	300
GTGCGTCGGC CTCAGCAAGC GCAAGTACCT CAGCGTCAGC TTCCGCCTCA ACCAGTCCGT	360
CGGCTTCAGC AAGCACAAGT GCGTCAGCCT CAGCAAGTAT CTCAGCGCTC GAATCGGCAT	420
CAACGAGTGC GTCTGAGTCA GCATCAACGA GTACGTCAGC CTCAGCAAGC ACATCAGCTT	480
CTGAATCTGC ATCAACCAGT GCGTCAGCCT CAGCATCGAC AAGCGCCTCA GCTTCAGCAA	540
GTACCAGTGC TTCAGCCTCA GCGTCGACAA GTGCGTCGGC CTCAACCAGT GCATCTGAAT	600
CGGCATCAAC CAGTGCCTCA	620

(2) INFORMATION FOR SEQ ID NO: 375:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 720 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

GTATTGGGGC GCCCCAACCT CTATGTGACT ACGGATTATT TCCTAGATTA CATGgGGATA	60
AACCATTAG AAGAATTACC AGTGATTGAT GAGCTTGAGA TTCAAGGCCA AGAAAGCCAA	120
TTATTTGGTG AAAGGATAGA AGAAGATGAG AATCAATAAG TATATTGCCC ACGCAGGTGT	180
GGCCAGTAGG AGAAAAGCAG AAGAGCTGAT TAAGCAAGGC TTGGTGACGG TAAACGGCCA	240
AGTGGTGCCT GAACTAGCAA CCACTATCAA GTCAGGCGAC AAGGTCGAAG TTGAAGGTCA	300
ACCTATCTAC AACGAAGAAA AGGTCTACTA TCTGCTTAAC AAACCACGCG GTGTGATTT	360
CAGTGTGACA GATGATAAGG GTCGCAAGAC GGTTGTCGAC CTCTTGCCCA ATGTCAAAGA	420
GCGTATTTC CCTGTGGGTC GTTGGACTG GGATACATCA GGTGTCTTGA TTTTGACCAA	480
TGATGGGGAC TTTACAGACG AGATGATTCA CCCTCGTAAT GAGATTGACA AGGTTTATGT	540
CGCGCGTGTAA AAAGGTGTGG CCAATAAGGA CAATCTCCGC CCCTTGACCC GTGGTCTTGA	600
GATTGATGGT AAGAAAACCA AGCCATAATA TATAGTTTT GTAGCCTCTA CACCATAAAT	660
ATTTGCTAAT AAAATACTG TATTATTACC CTCTTAAGGT GCGAAATTAT TCAAGTTCTT	720

(2) INFORMATION FOR SEQ ID NO: 376:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 648 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

CGCCATTCTC	CATCGTACCG	CCGAAATCC	CAGGCCCTCA	GCCATCAAAT	ATCCTATCAA	60
CGTTCTCAA	AAAAGTGACC	GCTCTCTCAT	CATGTTCCA	AGTGGTAGCC	GCCACTCAA	120
CGATGTCAAG	GGGGCGCAC	ACTskATTGC	CAAAATGGCC	AAGTCCGTA	TCATGCCGGT	180
TACCTACACC	GGTCCCAGTA	CTTTGAAGGG	CTTGATTAGC	CGTGAACGTG	TCGATATGAA	240
CTTTGAAAT	CCAATCGATA	TCTCAGATAT	CAAGAAAATG	AATGATGAAG	GCATTGAAAC	300
AGTCGCCAAT	CGTATTCAA	CAGAATTCCA	ACGCTGGAC	GAAGAAACGA	ACAAATGGCA	360
CAATGATAAA	AAACCAAATC	CACTCTGGTG	GTTTATCCGC	ATCCCTGCC	TCATCCTTGC	420
TATTATCCTC	GCTATCCTAA	CCATCATCTT	TAGCTTTATC	GCAAGCTTCA	TCTGGAACCC	480
AGATAAGAAA	AGAGAAGAAC	TTGCATAGAA	GAAATGAACC	TTGGCCAAAC	AGCTAAGGTT	540
TTCATTTATA	TAGTAGATTG	GwACTAGAAT	AGTACACCTC	TACTTCTAAA	ACATTTTAG	600
AAATCGATTT	GAATGTCCTG	ATCGATTTGT	CCTAATCTTA	TTTCAATT		648

(2) INFORMATION FOR SEQ ID NO: 377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 690 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

GTGCATCGCT	TTCAGCATCG	ACAAGTGCCT	CTGAATCGGC	ATCAACGAGT	GCTTCGGCTT	60
CAGCATCAC	GAGTGGTCA	GCTTCAGCAA	GCACATCAGC	TTCTGAATCT	GCATCAACCA	120
GTGCGTCCGC	TTCAGCGTCA	ACCAGTGCCT	CGGCTTCAGC	GTCGACAAGT	GCTTCGGCTT	180
CAGCATCAC	GAGTGGCTCG	GCCTCAGCAA	GCGCAAGTAC	CTCAGCGTCA	GCTTCGGCCT	240
CAACCACTGC	GTCCGTTCA	GCAAGCACA	GTGCGTCAGC	CTCAGCAAGT	ATCTCAGCGT	300
CTGAATCGGC	ATCAACGAGT	GCGTCGGCCT	CAGCAAGCGC	AACTACCTCA	GCGTCAGCTT	360
CCGCCTCAC	CAGTGGCTCG	GCTTCAGCAA	GCACAAGTGC	GTCAGCCTCA	GCAAGTATCT	420
CAGCGTCTGA	ATCGGCATCA	ACGAGTGCCT	CTGAGTCAGC	ATCAACGAGT	ACGTCAGCCT	480
CAGCAAGCAC	ATCAGCTCT	GAATCGGCAT	CAACCAGTGC	GTCAGCCTCA	GCATCGACAA	540
GCGCCTCAGC	TTCAGCAAGT	ACCAGTGCCT	CAGCCTCAGC	GTCGACAAGT	GCGTCGGCCT	600
CAACCAGTGC	ATCTGAATCG	GCATCAACCA	GTGCGTCAGC	CTCAGCAAGT	ACTAGTGCAT	660

1390
CAGCTTCAGC ATCAACGAGT GCATCGGCTT 690

(2) INFORMATION FOR SEQ ID NO: 378:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1003 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

CGAGATTCTC TGGAGTTATG GATCTCGTTC CAATATGTGC ACCTTGGAA	60
ATATGGGGGG AACAGAACATCC TCTCTTGATT GAAGACAAAGC TAGTCATTAG	120
CTTTTTGTCA ACTGTAGTGG GTTGATATAA TAGTATTAGT GAGTGGGATA AAAGTTTCAT	180
TTAGTTTATT CAGTACAAAT TTAACGGGTC AAGATTATA TACTAGTGGT GTTTTGGGG	240
CTGAGAGAAG TATCTTGATT TTATGTGTGG TTTTTACTACT TACAGTTGTT CTGCTCCAAA	300
GAGCTTGTAG AGAAGAATTA GCTCATAAAG GAGATTGATT ATTTTGATAT CAAAAAAATG	360
CACAGGATAA CCTGATGCAT TTTTTAGCG ACAATGCTTG CTACTTCCTT CTGTCGAATT	420
TAGACAATTT TAAACCCCAA TTATTCACCC CAAATCTAAA ACCATCCAG AATCCTTGCC	480
TTAGCTTACA TCCTGGATGG TTTCTTTTTT CACCAATGG GTGTTTTTA CTAGACAAAA	540
AAGAGTTCC CTTTTATGGT ATAAGTGTAG AAAAAAACAC AAAAAAGAAAG GAAACTCACA	600
TGAACAGTTT ACCAAATCAT CACTTCCAAA ACAAGTCTTT TTACCAACTA TCTTTCGATG	660
GAGGTCATTT AACCCAGTAT GGTGGTCTTA TCTTTTTCA GGAACTTTTT TCCCAGTTGA	720
AACTAAAAGA GCGGATTTCT AAGTATTTAG TAACGAATGA CCAACGCCGC TACTGTCGTT	780
ATTCGGGATTC AGATATCCTT GTCCAGTTCC TCTTTCAACT GTTAACAGGT TATGGAACGG	840
ACTATGCTTG TAAAGAATTG TCAGCTGATG CCTACTTTCC AAAATTATTG GAAGGAGGGC	900
AGCTTGCTTC ACAGCCAACC TTATCCCGTT TTCTTTCCAG AACTGACGAG GAAACAGTCC	960
ATAGTTGCG ATGCCCTAAC CTTGAATTGG TCGAATTCTT TTT	1003

(2) INFORMATION FOR SEQ ID NO: 379:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 738 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

1391

CCGATGATTG	TGATTGGTTT	GCTCTTACT	TTGCTGGAA	TTTTGAGGTA	GATCTATGAT	60
TGAAATACTA	ATTGTTTAG	CTATTATCCT	ATCTCTTGCT	TTGATTGTAT	TGGTAACTAT	120
ACAACCCCGT	CAAAATCAAC	TATTTCCAT	GGATGCCACT	AGTAATATTG	GTAAACCAAG	180
CTACTGGCAG	AGCAACACCT	TGGTCAAGGT	GCTCACTTA	TTGGTGAGTT	TGGCTTTATT	240
TATTCTACTA	TTAACCTTA	TGGTGATTAC	TTATAAATAA	AAGAAAAC	CAGATATTCA	300
CCTTTGTTG	ATTGGTCTGA	AGTTTTCTTT	TTTATACTCA	ATGAAAATCA	AAGAGCAAAC	360
TAGGAAGCTA	GCCGCACkGC	TCAAAACACC	GTGAGGTT	TGTAGATATA	ACTGACGAGC	420
GACTCAAAAC	ACCGTTTGA	GGTTGTAGAT	ATAACTGACG	AGGACTCAA	AAACCCGTTT	480
TGAGGTTGTG	GATAGAACTG	ACGAGGACT	CAAAACACCG	TTTGAGGTT	GTGGATAGAA	540
CTGACGAAGT	CGcTCAAAAC	ACCGTTTGA	GGTTGTGGAT	AGAACTGACG	AATgtcAAA	600
ACACCGTTT	GAGGGTTG	ATAGAACTGA	CGAAGCgaaC	ATATATACAG	CAAGGGGACG	660
CTGACGTGGT	TTGAAGAGTA	TTACTGTCTA	TATTTTGTT	AAAAATCAAC	TTTTACTTGG	720
ATGAAGGTTT	TTTTTTTT					738

(2) INFORMATION FOR SEQ ID NO: 380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 695 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

CCGTCTTATC	AAAGAGGTTA	ACAAAGGCAC	CAAATTTCTC	GATACGAACG	ACTTTAGCAC	60
GGTAAACTTC	ATCCACTTG	GCTTCACGAA	CCAACCAGC	AATAATTCT	TTGGCACGGT	120
TAATAGCATC	TTGGTCACTA	GAGTAGATAG	ACACATTCC	TTCTTCGTCT	ATATCAATCT	180
TAACACCTGT	TTCAGCGATA	ATCTTGTGCA	TGGTTCTCC	ACCCCTACCG	ATGACAATCT	240
TAATCTTGTC	CACATCAATC	TTGATCGTAT	CAATTTCGG	AGCAGTTGGA	GCCAATTCTG	300
GACGAACTTC	TGGAATGGTT	GCTTCATGA	CATCAAGGAT	TTCAAAACGC	GCTTTCTTGG	360
CTTGAGGCAAG	AGCCTCCGTC	AAGATTCTG	CAGTAATCCC	TTGAATCTTG	ATATCCATT	420
GAAGGGCTGT	AATCCCATCA	CGAGTACCTG	CAACCTTGAA	GTCCATATCT	CCAAAGTGAT	480
CTTCCAAACC	TTGGATATCT	GTCAAACTG	TGTAGTTATT	TCCATCTGAG	ATAAGCCCCA	540
TAGCAATACC	AGCTACTGGC	GCCTTGATTG	GCACACCACC	AGCCATAAGG	GCAAGAGTTC	600

1392	
CCGCACAGAT AGAACGTTGA GATGAAGAAC CGTTGATTC CAAAACCTCT GCTACTAGAC	660
GGATAGCGTA GGGGAATTCT TCCAAGCTTG GCAGG	695

(2) INFORMATION FOR SEQ ID NO: 381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 691 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

GACATCTTAT CTAAATACAT GCTAATATAT TTAGATACAA ACATTCCAAC TTGATAATTT	60
TCACTCATCT TTCATCATTC CTTATACAAAC TATGCACTAT AAATAGAATA GTTTTCTCAT	120
CAGAATGAGA CTATTTAAT ATTAGATCCC CAATTATTCA CCCAAATCT AAAAACCATC	180
CAGAACCTCT GCCTTAGCTT AGATCCTGGA TGTTTCTTT TTTCACCCAA TGGGTGTTT	240
TTACTAGACA AAAAGAGTT TCCCCTTTAT GGTATAAGTG TAGAAAAAAA CACAAAAAGA	300
AAGGAAACTC ACATGAACAG TTTACCAAAT CATCACTTCC AAAACAAGTC TTTTACCAA	360
CTATCTTCG ATGGAGGTCA TTTAACCCAG TATGGTGTC TTATCTTTT TCAGGAACCTT	420
TTTCCAGT TGAAACTAAA AGAGCGGATT TCTAAGTATT TAGTAACGAA TGACCAACGC	480
CGCTACTGTC GTTATTCGGA TTCAGATATC CTTGTCCAGT TCCCTTTCA ACTGTTAACCA	540
GGTTATGGAA CGGACTATGC TTGTAAGAA TTGTCAGCTG ATGCCTACTT TCCAAATTG	600
TTGGAAGGAG GGCAGCTTGC TTCACAGCCA ACCTTATCCC GwTTTCTTT CAGAACTGAC	660
GAGGAAACAG TCCATAGTTT GCGATGCCTC A	691

(2) INFORMATION FOR SEQ ID NO: 382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

ATCTCTCTGC GAAATGGTCC TCAGATAACT CTGATGATGT GTGGCGATAT AGAACTGAGC	60
CAAGTTATGC CTAAAGGGCC TTAGGAATAG GAGCTTCAC AAGCTTATCC AGATGATTAT	120
CTTTTACTCG TTATGGACAA TGCTATATGG CATAATCAA GTACCTTAAA GATTCCGACT	180
AATATTGGCT TTGCATTTAT TCCTCCATAC ACACCAGAGA TGAACCCAT TGAACAAAGTG	240

1393

TGGAAAGAGA	TTCGTAACG	TGGATTAAAG	AATAAAGCCT	TTCGAACATT	GGAAGATGTC	300
ATACAAGGAC	TGGAGAAGGA	GGTGATAAAG	TCCATCGTTA	ATCGGAGACG	GACTAGAATG	360
CTTTTTGAAA	ACAGATGAGT	ATAAAAAAGAA	AGTCCTCATT	TCAATAGAAA	TCACGACTTT	420
CTGATGAATT	TATAGTAAAA	TGAAATAAGA	ACAGGGATAGT	CAAATCGATT	TCTAACAAATG	480
TTTTAGAACG	AGAGGTGTAC	TATTCTAGTT	TAATTCACACT	ATATTGGGG	AGTGTAGAGAA	540
AAGCCCTTCA	TCAGCCAATC	TACTTGTCA	GGTGGAGAG	CTTTGACATC	CTTTCTGTAA	600
CTGGACCAAG	TCAGTTTCC	GTTCTCAAAG	CGTTTATATA	ATATCCAAA	TCCTTGACCA	660
TCCCAGTAAA	GAACTTAAA	GCGGTCTTCA	CGTCCACAC	AAAAGAGAAA	GACTTGTACG	720
GAGAAAGGAT	CCAATTCAAA	GTGGGTTTGG				750

(2) INFORMATION FOR SEQ ID NO: 383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 738 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

TCAAATTCTT	CGTGGTCCGC	ATATCThtCT	TCGTACACGG	CACTCACTTG	GTCTTTCACT	60
ACTCGAGTCG	CAGCTTCACG	GGCCAATPTC	TCTTCTACTT	GAAC TGCC TT	TTGGAGGTCA	120
CTGTTGTTAGG	CTGCAATGAT	TTCA GCTTGC	AATT CAGCAT	CCAC GTGAAG	CAATTCCACT	180
TCTGCTTTTT	CTTTACCGAC	AGCAGCAACG	ATTTCTTCTT	GGAGGCAAT	CAATTCTTG	240
ACAGCTTCGT	GCCCTTTAAG	GAGC GCTTCC	AAACATGATTT	CTTCTGACAA	TTCTTGGCA	300
CCAGACTCTA	CCATGTTGAT	AGCGTGCCTG	GTTCCAGCTA	CTGTCATTC	AAGAAGAGAT	360
TGCTCTGCTT	GTTCTTGACT	TGGGTTGATG	ATGATTTGGC	CATCTACATA	TCCCACTTGT	420
ACCCCAGCAA	TTGGTCCGTC	AAATGGAATA	TCTGAAATAG	ACAGTGCCAA	AGATGAACCA	480
AACATAGCAG	CCATTGGTGC	AGATGCATTT	TCATCATAAG	AAAGCACTGT	ATTGTGACT	540
TGGACTTCAT	TACGGAAACC	TTCCGCAAAC	ATAGGACGAA	TCGGACGGTC	AATCAAACGC	600
GCTGTCAAGG	TCGCATCTGT	TGAAGGACGT	CCTTCACGTT	TCATAAAGCC	ACCAGGAAAC	660
TTCCCAGCCG	CATACATTTT	TTCTTCGTAG	TTGACTTGGA	GTGGGAAGAA	ATCCTCAGTT	720
GCCATTTCT	GGGGATCC					738

(2) INFORMATION FOR SEQ ID NO: 384:

1394

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 657 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

CCCCCTATTT ACCGTGGACT AAAGTTGTAC AAGAAAAGTG CAAATAAGAA ATCTCCAGAT	60
TAGGAACTAT ATATGAGTTC TCTAGTCTGG AGATTTTCAGA ATAGACTTCG TTATTGGGCG	120
GTTACTTTCG AAACCTTGAA AACTCAAAA AACGGATTTT TATCGCTTTC AAATTCTTT	180
GGGGTCAAAC TCAGTAACTT ATTTCGCTTG TAGACTTCAT GACGCTCAGG GTATACTTTC	240
AAGGTCCCAA ATAGCCAAGA ATCGTCAGCG ATATTATCTG AATCATCTCC TTCTTGTTCT	300
CCTTCTAGTTC GCCTGAGGAC AGCCCTTGACA CGCGCCAGAA TTCTCTAGGG CTAAAAGGCT	360
TGGTCAGGTA GTCATCAGCC CCTAATTCCA AGGCCAAAC CTTATCAAAT TCATCACTTT	420
TCGCAGAAAC CATCATAATT GGAGTTTGAGA CGCCCTTGCG TCTCAGCCGC TTACAAACTT	480
CCATGCCATC TAATTGTGGT AACATGATAT CAAGCAAGAT AAAATCAAAG GGTTCTGTTT	540
CTGCCAAAGC TAAGGCCATC CGTCCATTG TCACCAATTG AGTAGAAAAG CCTTCCTTAC	600
TTAAATGGTA GTCAAGCAAT TTCAAGATGT GTTCTTCATC ATCCACTAAT AAGACTT	657

(2) INFORMATION FOR SEQ ID NO: 385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 586 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

CCGCATCAGC ATCAACGAGT GCATCGGCTT CACGTCAACC AGTGCATCAG TCTCAGCAAG	60
CACCAAGTGGC TCGGCTTCAG CATCAACGAG TGCGCTCAGCC TCAGCAAGTA TCTCAGCGTC	120
TGAATCGGCA TCAACGAGTG CGTCAGCTCA GCAAGTACTA GTGCATCGGC TTCAGCAAGC	180
ACCAGTGCCT CGGCTTCAGC ATCAACCGAT GCCTCAGCCT CAGCAAGTAT CTCAGCGTCT	240
GAATCGGCAT CAACGAGTGC GTCACCTCAG CAAGTACTAG TGCAATCAGCA TCAGCATCAA	300
CGAGTGCATC GGCTTCAGCA AGTACCAAGCG CCTCAGCTTC AGCAAGCACC AGTGCCTCAC	360
CTCAGCAAGT ACCAGCGCCT CAGCCTCAGC AAGCACCAGT GCCTCAGCTT CAGCAAGTAC	420
CAGTGCCTCA CCTCAGCATC GACAAGTGCG TCGGCTTCAG CAAGTACCTC AGCGTCTGAA	480

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TCAGCATCAA CGAGTGCAGTC AGCTTCAGCA TCAACCAGTG CCTCAGCCTC AGCAAGTATC	540
AGTGCCTCAG CTTCACCATC AACGAGTGCAG TCAGCTGCAG CAAAGT	586

(2) INFORMATION FOR SEQ ID NO: 386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

CGTCGGCTTC AGCATCAACG AGTGCATCAG CTTCAGCAGC AACAAAGTGCT TCAGCTTCAG	60
CAAGTACAG TGCCTCGGCT TCAGCATCAA CGAGTGCAGTC AGTCTCAGCG TCAACCAGTG	120
CCTCTGAATC CGCATCAACA AGTGCCTCGG CTTCAGCAAG CACCAGTGCT TCGGCTTCAG	180
CGTCAACGAG TGCGCTCTGAG TCAGCATCAA CGAGTGCAGTC ACCTCAGCAA GCACATCAGC	240
TTCTGAATCT GCATCAACCA GTGCCTCAGC TTCCCCATCA ACAAGCGCCT CGGGCTCAGC	300
AAGTACAAGT GCTTCAGCCT CAGCATCAAC CAGTGCATCA GCTTCAGCCT CAACAAGTGC	360
TTCAGCCTCA GCGTCAACCA GTGCCTCGGC TTCAAGCAAGT ACCAGTGCAGT CAGTTcAGCA	420
AGCACAAAGTG CGTCAATTAA GCATCAACCA G	451

(2) INFORMATION FOR SEQ ID NO: 387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

TCTCAGCAAG CACCATTGCG TCGGCTTCAT CAAGCACCAAG CGCGTTGAA TCCGCATCAA	60
CCAGTGCTTC AGCTTCAGCC AAGTTACCTC AGCATCTGAA TCAGCATCAA CAAGTGCATC	120
GGCTTCAGCA AGCACAAAGTG CTTCAGCTCA GCAAGTATCT CAGCGTCTGA ATCGGCATCA	180
ACGAGTGCAGT CGCGCTTCAGC AAGTACTAGC GCCTCAGCAT CAGCGTCAAC AAGTGCCTCG	240
GCTTCAGCGT CAACGAGTGC GTCTGAGTCA GCATCAACGA GTACGTAGC CTCAGCAAGC	300
ACATCAGCTT CTGAATCTGC ATCAACCAGT GCGTCAGCCT CAGCATCGAC AAGCGCCTCA	360
GCTTCAGCAA GTACCAGTGC GTCAAGCCTCA GCAAGTACCA GTGCTTCAGC CTCAGCGTCG	420

1396

ACAAG

425

(2) INFORMATION FOR SEQ ID NO: 388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

AGAGGATCCC CGGATCCTCA GTCGCTGAGA TAACTCCTTT GGGCTTGTTC ATCATGTAGT	60
AGACAAACTC TTCATACTCC AACACTTGCC CATTATGTC GAATCTCATC TATTTTTTCT	120
TTTTTTGCA ATTTAGCTGA TTTTCTTTT TTACCATTTA CAGTCACGCG CCCAGCCTG	180
AGCAAGTTT TGACCTCAGT CCGACTTCCC ACCGCACAGG CAACTAAAAA TTTATCTAAT	240
CTCATAGAAC TATTATATCA TATCAAAAGG AGGCTAGTAC AATGACCAAC CTCCCTTTCG	300
TTTCATACTC TTCAAAATC TCTTCAAAACC GCGTCAACGT CGCCTTGCCG TATATATGTT	360
ACTGACTTCG TCAGTTCTAT CTGCAACCTC AAAACAGTGT TTTGAGCTGA CTTCGTCAGT	420
TCTATCTGCA ACCTCAAAGC AGTGCTTGA GCATCCTGCG GCTAGTTCC kAGTktGCTC	480
TTTGATTTwc ATTGAGTATC AGATTAGGA AATTAACTTC CTCGkCTCCA AAAAAkAGCT	540
AAAACAATCA AGGCTCCTAA AATCGCTGGG AT	572

(2) INFORMATION FOR SEQ ID NO: 389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

CAACAAGTGC CTCGGCTTCA GCATGCACAA GTGCTTCAGC TTCAGCATGT ACCTGAGCGT	60
CTGAATCAGC ATCAACGTGT GCGTCCGCTT CAGCATGTAC TGCTGCCTCA GCATCAGCGT	120
CAACAwGTGC TTCGGCTTCA GCGTCAACGA GTGCGTCTGA GTCAGCATCA ACGAGTACGT	180
CAGCCTCAGC AAGCACATCA GCTTCTGAAT CTGCATCAAC CAGTGCCTCA GCCTCAGCAT	240
CGACAAGCGC CTCAGCTTCA GCAAGTACCA GTGCGTCAGC CTCAGCAAGT ACCAGTGCTT	300
CAGCCTCAGC GTCGACAAGT GCGTCGGCCT CAACCAGTGC ATCTGAATCG GCATCAACCA	360
GTGCGTCAGC CTCAGCAAGT ACTAGCGCCT CAGCCTCAGC ATCAACGAGT GCGTCCGCTT	420

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CAGCAAGTAC TAGTGCATCA GCATCAGCAT CAACGAGTGC ATCGGCTTCA GCAAGTACCA	480
GCGCCTCAGC TTCAGCAAGC ACCGG	505

(2) INFORMATION FOR SEQ ID NO: 390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

GCTAAAGACTA CCTCATTAGG GGCATAGGCT GCTAAAATAA CTGCAGCTGT GGTTAATGAC	60
AATACTGTAC TTTTTTTCAT TTTAATTCCCT TACATATTAA TATAACTTCC AATAGATAAT	120
AAACTTTAAC TTTGCTAGCC TTTGTTATAA AAAGTTTAC TAAGTATTAT CTAGGAAATA	180
GAGTAGTACA TTTATATATA ATTGTTATCT CTCTATAAAA ACAGTATATC ATTTAAAAAA	240
ATTTAACTCA AAAAAATTAAC CATTAGTTAA TTTATTTTTT AGCACACATT AAAAAATAAG	300
ATTAGTACTC AATGAAAATC AAAGAGCAAA CTAGGAAACT AGCCGCAGAT TGCTAAAAAC	360
AGTGTGTTGA GGTGTTAGAT GGAATGACGT AGTCAGCTCA AAACACTGTT TTGAAGTTGT	420
GGATAGAACT GACGAAGTCG GTACCGA	447

(2) INFORMATION FOR SEQ ID NO: 391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

AGCACTTGTC GTTGAATTCT ACAACAAAAT GTTGTAAATAT TTTATTGAAT AAGATAGGCC	60
TTGATATTAA GCACTTTGGG ACGTTCTCCC TTAGTGCTTT TTTGATTCT CTTAGTATCC	120
AGCTATAATC GTTGAGACAT AACTAGACCG ATATAGTCCA AAGTGATATA GTAAAATGAA	180
CCAAAAATAG TACACAATGT GGTATAATCC TTTTATGGCA TATTCAATAG ATTTTCGTAA	240
AAAAGTTCTC TCTTATTGTG AGCGAACAGG TAGTATAACA GAAGCATCAC ACGTTTTCCA	300
AATCTCACGT AATACCATTG ATGGCTGGTT AAAGCTAAAA GAGAAAACAG GAGAGCTAAA	360
CCACCAAGTA TAGTGTATTG AATCTATAAC AGTACACCTT GGCTGCTAAA ATATTTCTAT	420

1398	
AAATTAATTT GACTTTCCCTG ATAGAGATGT TCACATCTTA TTTCAAACTA CTATATAAGT	480
TCTATAATCT CTTTATAAAGA TTTGCCCATC AGACAAAATA GAACGATTG AAGGCCTTTA	540
TGATATTTAG CTGTACGAGA GTCTTTAAA AG	572

WO 98/18931

PCT/US97/19588

1399

MISSING UPON TIME OF PUBLICATION

1400

DENMARK

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person approved by the applicant in the individual case.

SWEDEN

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PUT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant, any request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent Office or any person approved by the applicant in the individual case.

UNITED KINGDOM

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the International publication of the application.

NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapse, the microorganism shall be made available as provided in Rule 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever two dates occurs earlier.

SINGAPORE

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for international publication of the application.

NORWAY

The applicant hereby requests that, until the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

AUSTRALIA

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Registration), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

ICELAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the Icelandic Patent Office), or has been finally decided upon by the Icelandic Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected in the art.

What Is Claimed Is:

- 25 1. Computer readable medium having recorded thereon the nucleotide sequence depicted in SEQ ID NOS:1-391, a representative fragment thereof or a nucleotide sequence at least 95% identical to a nucleotide sequence depicted in SEQ ID NOS:1-391.
- 30 2. Computer readable medium having recorded thereon any one of the fragments of SEQ ID NOS:1-391 depicted in Tables 2 and 3 or a degenerate variant thereof.
- 35 3. The computer readable medium of claim 1, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.
- 40 4. The computer readable medium of claim 3, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.
- 45 5. A computer-based system for identifying fragments of the *Streptococcus pneumoniae* genome of commercial importance comprising the following elements:
 - a) a data storage means comprising the nucleotide sequence of SEQ ID NOS:1-391, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS:1-391;
 - b) search means for comparing a target sequence to the nucleotide sequence of the data storage means of step (a) to identify homologous sequence(s), and
 - c) retrieval means for obtaining said homologous sequence(s) of step (b).
- 50 6. A method for identifying commercially important nucleic acid fragments of the *Streptococcus pneumoniae* genome comprising the step of comparing a database comprising the nucleotide sequences depicted in SEQ ID NOS:1-391, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS:1-391 with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence is not randomly selected.

60 7. A method for identifying an expression modulating fragment of
 Streptococcus pneumoniae genome comprising the step of comparing a database
 comprising the nucleotide sequences depicted in SEQ ID NOS:1-391, a
 representative fragment thereof, or a nucleotide sequence at least 95% identical to
 the nucleotide sequence of SEQ ID NOS:1-391 with a target sequence to obtain a
65 nucleic acid molecule comprised of a complementary nucleotide sequence to said
 target sequence, wherein said target sequence comprises sequences known to
 regulate gene expression.

70 8. An isolated protein-encoding nucleic acid fragment of the *Streptococcus*
 pneumoniae genome, wherein said fragment consists of the nucleotide sequence of
 any one of the fragments of SEQ ID NOS:1-391 depicted in Tables 2 and 3, or a
 degenerate variant thereof.

75 9. A vector comprising any one of the fragments of the *Streptococcus*
 pneumoniae genome SEQ ID NOS:1-391 depicted in Tables 2 and 3 or a
 degenerate variant thereof.

80 10. An isolated fragment of the *Streptococcus pneumoniae* genome,
 wherein said fragment modulates the expression of an operably linked open reading
 frame, wherein said fragment consists of the nucleotide sequence from about 10 to
 200 bases in length which is 5' to any one of the open reading frames depicted in
 Tables 2 and 3 or a degenerate variant thereof.

85 11. A vector comprising any one of the fragments of the *Streptococcus*
 pneumoniae genome of claim 8.

12. An organism which has been altered to contain any one of the
 fragments of the *Streptococcus pneumoniae* genome of claim 8.

90 13. An organism which has been altered to contain any one of the
 fragments of the *Streptococcus pneumoniae* genome of claim 10.

95

14. A method for regulating the expression of a nucleic acid molecule comprising the step of covalently attaching to said nucleic acid molecule a nucleic acid molecule consisting of the nucleotide sequence from about 10 to 100 bases 5' to any one of the fragments of the *Streptococcus pneumoniae* genome depicted in SEQ ID NOS:1-391 and Tables 2 and 3 or a degenerate variant thereof.

100

15. An isolated nucleic acid molecule encoding a homolog of any of the fragments of the *Streptococcus pneumoniae* genome of SEQ ID NOS:1-391 and Tables 2 and 3, wherein said nucleic acid molecule is produced by a process comprising steps of:

105

- a) screening a genomic DNA library using as a probe a target sequence defined by any of SEQ ID NOS:1-391 and Tables 2 and 3, including fragments thereof;
- b) identifying members of said library which contain sequences that hybridize to said target sequence; and
- c) isolating the nucleic acid molecules from said members identified in step (b).

110

16. An isolated DNA molecule encoding a homolog of any one of the fragments of the *Streptococcus pneumoniae* genome of SEQ ID NOS:1-391 and Tables 2 and 3, wherein said nucleic acid molecule is produced a process comprising steps of:

115

- a) isolating mRNA, DNA, or cDNA produced from an organism;
- b) amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from said fragment of said *Streptococcus pneumoniae* genome to prime said amplification;
- c) isolating said amplified sequences produced in step (b).

120

17. An isolated polypeptide encoded by any of the fragments of the *Streptococcus pneumoniae* genome of SEQ ID NOS:1-391 and depicted in Table 2 and 3 or by a degenerate variant of said fragments.

125

18. An isolated polynucleotide molecule encoding any one of the polypeptides of claim 17.

19. An antibody which selectively binds to any one of the polypeptides of
claim 17.

130

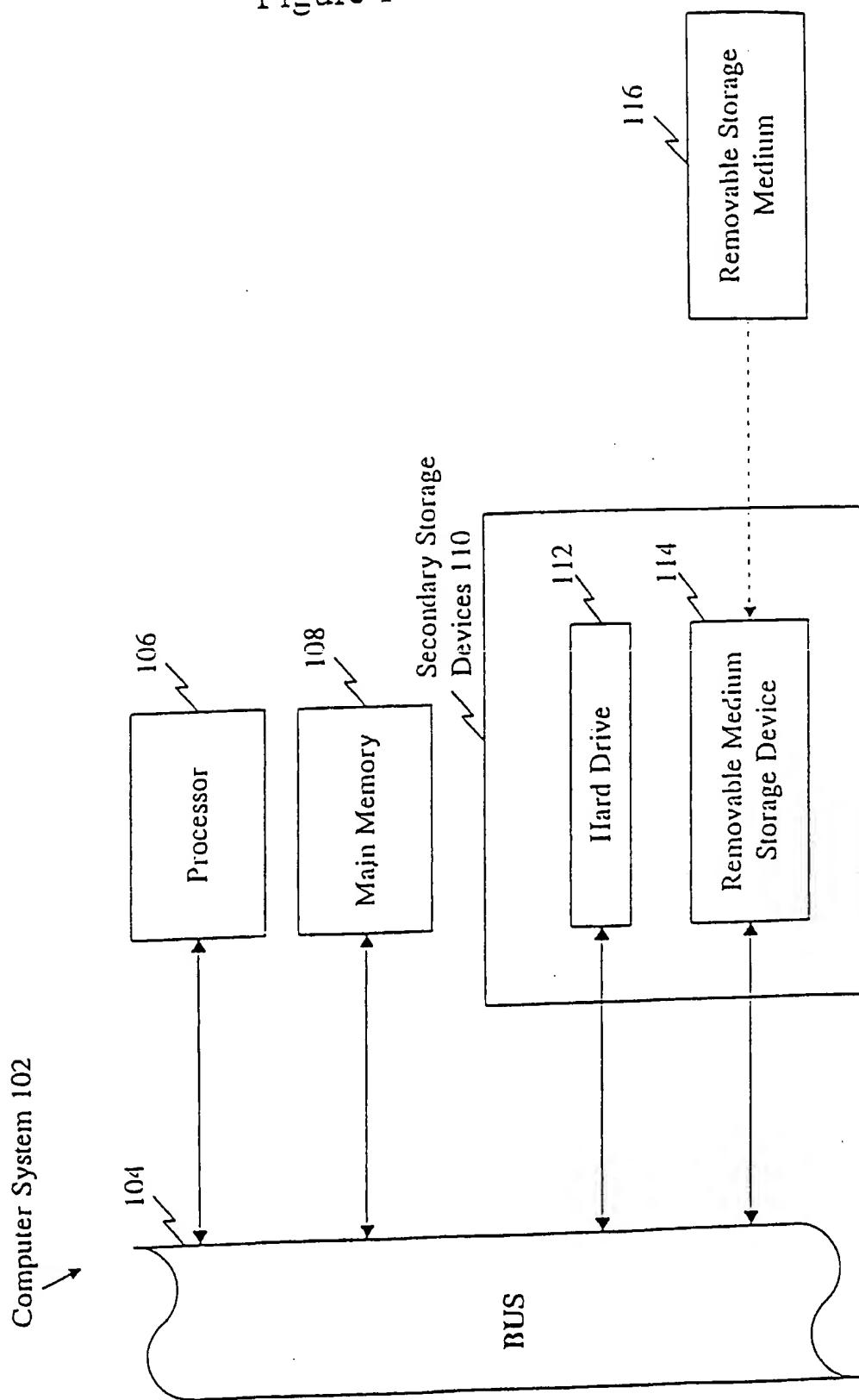
20. A method for producing a polypeptide in a host cell comprising the
steps of:

135

a) incubating a host containing a heterologous nucleic acid molecule whose
nucleotide sequence consists of any one of the fragments of the *Streptococcus*
pneumoniae genome of SEQ ID NOS:1-391 and depicted in Tables 2 and 3, under
conditions where said heterologous nucleic acid molecule is expressed to produce
said protein, and

b) isolating said protein.

Figure 1



AGTGCTTCAG TCTCAGCGTC AACCAAGTGC C TCTGAATCAG CATCAACAAG TGCCTCGGCT	1384	900
TCAGCAAGCA CCAGTGGCGTC GGCTTCAGCA AGTACTAGTG C		941

(2) INFORMATION FOR SEQ ID NO: 369:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 869 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

CAGCAAGTAC TAGTGCATCA GCTTCAGCAT CAACGAGTGC ATCGGCTTCT GCGTCAACCA	60
GTGCATCAGA GTCAGCAAGT ACCAGTGCCT CAGCTTCCGC ATCAACAAGT GCCTCGGCTT	120
CAGCAAGCAC CAGTGCCTCG GCTTCAGCAA GTACTAGCGC CTCAGCCTCA GCCTCAACCA	180
GTGCGTCAGC CTCAGCAAGT ATCTCAGCGT CTGAATCGGC ATCAACGAGT GCGTCCGCTT	240
CAGCAAGTAC TAGCGCCTCA GCCTCAGCGT CAACAAGTGC ATCGGCTTCA GCGTCAACGA	300
GTGCGTCTGA ATCGGCATCA ACGAGTGCCT CCGCTTCAGC AAGTACTAGC GCCTCAGCCT	360
CAGCGTCAAC AAGTGCATCG GCTTCAGCAT CAACGAGTGC GTCCGCTTCA GCAAGTACTA	420
GCGCCTCAGC CTCAGCGTCA ACAAGTGCAT CGGCTTCAGC GTCAACGAGT GCGTCTGAGT	480
CAGCATCAAC GAGTGCCTCA GCCTCAGCAA GCACATCAGC TTCTGAATCT GCATCAACCA	540
GTGCGTCAGC CTCAGCATCG ACAAGCGCCT CAGCTTCAGC AAGTACCGAGT GCGTCAGCCT	600
CAGCGTCGAC AAGTGCCTCG GCTTCAGCAA GTACCGAGTGC GTCAGCCTCA GCAAGTACCA	660
GTGCGTCAGC CTCAGCGTCA ACAAGTGCCT CAGCTTCAGC AGTGCATCT GAATCGGCAT	720
CAACCAAGTGC GTCAGCCTCA GCAAGTACTA GTGCATCAGC TTCAGCATCA ACGAGTGCAT	780
CGGCTTCAGC ATCAACCAGT GCATCAGAGT CAGCAAGTAC CAGTGCCTCA GAGTTCCGCAT	840
GCAACAAGTG CCTCGGCTTC AGCAAGTAC	869

(2) INFORMATION FOR SEQ ID NO: 370:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 750 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

TCAACAAGTG CCTCAGCATC AGCATCAACG AGTGCCTCG CTCAGCAAG TACTAGTGCA	60
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1385

TCAGCATCAG CATCAACCAAG TGCATCAGCC TCAGCAAGTA TCTCAGCGTC TGAATCGGCA	120
TCAACGAGTG CATCAGCATC AGCATCAACG AGTCATCGG CTTCAGCGTC AACCAAGTGCA	180
TCAGTCTCAG CAAGCACCAG TGCCTCGGCT TCAGCATCAA CGAGTGCCTC AGCCTCAGCA	240
AGTATCTCAG CGTCTGAATC GGCATCAACG AGTGCAGTCAG CCTCAGCAAG TACTAGTGCA	300
TCGGCTTCAG CAAGCACCAG TGCCTCGGCT TCAGCATCAA CGAGTGCCTC AGCCTCAGCA	360
AGTATCTCAG CGTCTGAATC GGCATCAACG AGTGCAGTCAG CCTCAGCAAG TACTAGTGCA	420
TCAGCATCAG CATCAACCAAG TGCATCGGCT TCAGCAAGTA CCAGCGCCTC AGCTTCAGCA	480
AGCACCAAGTG CGTCAGCCTC AGCAAGTACG AGCCGCCTCAG CCTCAGCAAG CACCAAGTGCC	540
TCAGCTTCAG CAAGTACCAAG TGCCTCAGCC TCAGCGTCGA CAACTGCAGTC GGCTTCAGCA	600
AGTACACTCAG CGTCTGAATC AGCATCAACG AGTCATCAG CTTCAGCATC AACAAAGTGCT	660
TCAGCTTCAG CAAGTATCTC AGCGTCTGAA TCGGCATCAA CGAGTGCAGTC CGCTTCAGCA	720
AGTACTAGCG CCTCAGCATC AGCGTCAACG	750

(2) INFORMATION FOR SEQ ID NO: 371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 957 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

CCGGAAAACA GCTCTGGCGC TTGGTCTTGC CCAGCGTATT GCTAGTGGTG ACGTGCCTGC	60
GGAAATGGCT AAGATGCGCG TGTAGAAACT TGATTTGATG AATGTCGTTG CAGGGACACG	120
CTTCCGTGGT GACTTGAAAG AACGCATGAA TAATATCATC AAGGATATTG AAGAAGATGG	180
CCAAGTCATC CTCTTATCG ATGAACCTCA CACCATCATG GGTTCTGGTA CGGGGATTGA	240
TTCGACTCTG GATGCGGCCA ATATCTTGAA ACCAGCCTTG CGCGGTGGAA CTTTGAGAAC	300
GGTTGGTGCC ACTACTCAGG AAGAATATCA AAAACATATC GAAAAAGATG CGGCACTTTC	360
TCGTCGTTTC GCTAAAGTGA CGATTGAAGA ACCAAGTGTG CGAGATAGTA TGACTATTT	420
ACAAGGTTG AAGGCGACTT ATGAGAAACA TCACCGTGT ACAAATCACAG ATGAAGCGGT	480
TGAAACAGCG GTTAAGATGG CTCATCGTTA TTTAACCAAGT CGTCACCTGC CAGACTCTGC	540
TATCGATCTC TTGGATGAGG CGGCAGCAAC AGTGCAAAAT AAGGCAAAGC ATGTAAAAGC	600
AGACGATTCA GATTGAGTC CAGCTGACAA GCCCCTGATG GATGGCAAGT GGAAACAGGC	660

AGCCCAGCTA ATCGCAAAAG AAGAGGAAGT ACCTGTCTAC AAAGACTTGG TGACAGAGTC	1386 720
TGATATTTG ACCACCTTGA GTCGCTTGTC AGGAATCCCA GTTCAAAAAC TGACTCAAAC	780
GGATGCTAAG AAGTATTTAA ATCTTGAAGC AGAACTCCAT AAACGGGTTA TCGGTCAAGA	840
TCAAGCTGTT TCAAGCATT A GCCGTCAC TCGCCGCAAC CAGTCAGGGA TTTCGCACTCA	900
TAAGCGTCCG ATTCGGTTCCCT TTATGTTCCCT AGGGCCTACA GGTGTCGGGG TATCCGA	957

(2) INFORMATION FOR SEQ ID NO: 372:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 807 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

CAAAGCGCCT CAGCTTCAGC ATCAACAAGT GCGTCGGCTT CAGCATCAAC CAGTGCCTCG	60
GCTTCAGCGT CAACCAGTGC GTCACATTCA GCAAGTACCA GTGCTTCAGT CTCAGCATCA	120
ACAAGTGCTT CAGCCTCAGC ATCGACAAGT GCCTCGGCTT CAGCAAGCAC ATCAGCATCT	180
GAATCAGCGT CAACCAGTGC TTTCGGCTTC GCAAGTACCA GTGCTTCAGC TTTCAGCATCA	240
ACCAAGGCGCT CGGCCTCAGC AAGCACCTCA GCTTCTGAAT CGGCCTCAAC CAGCGCCTCG	300
GCCTCAGCAA GCACCTCAGC TTCTGAATCG GCCTCAACCA GCGCCTCAGC CTCAGCATCA	360
ACGAGTGCTT CGGCTTCAGC AAGCACAAAGC GCCTCGGGTT CAGCATCAAC GAGTACGTCA	420
GCTTCAGCGT CAACCAGTGC TTCAGCCTCA GCATCAACAA GTGCGTCAGC CTCAGCAACT	480
ATCTCAGCGT CTGAATCGGC ATCAACGAGT GCGTCTGAGT CAGCATCAAC GAGTACGTCA	540
GCCTCAGCAA GCACCTCAGC TTCTGAATCG GCCTCAACCA GTGCGTCAGC CTCAGCATCG	600
ACAAGCGCCT CAGCTTCAGC AAGTACCAAGT GCTTCAGCCT CAGCGTCGAC AAGTGCCTCG	660
GCCTCAACCA GTGCATCTGA ATCCGGCATCA ACCAGTGCAGT CAGCCTCAGC AAGTACTAGT	720
GCATCGGCTT CAGCATCAAC CAGTGCCTCG GCTTCAGCGT CAACCAAGTGC GTCAGCTTC	780
GCAAGTACCA TGTGCTTCAT GTCTCAG	807

(2) INFORMATION FOR SEQ ID NO: 373:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1068 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

CATCGGCTTC AGCATCAACG AGTGGTCCG CTTCAAGCAAG TACTACCGCC TCAGCCTCAG	60
CGTCAACAAG TGCATCGGCT TCAGCGTCAA CGAGTGCCTC TGAGTCAGCA TCAACGAGTG	120
CGTCACCTCA GCAAGCACAT CAGCTTCTGA ATCTGCATCA ACCAGTGCCTG CACCTCAGCA	180
TCGACAAGCG CCTCAGCTTC AGCAAGTACG AGTGCCTCAC CTCAGCGTCA ACAAGTGCCTG	240
CGGCTTCAGC AAGTACCAAGT CGGTCAAGCTC AGCAAGTACG AGTGCCTCAC CTCAGCGTCA	300
ACAAGTGCCTG CGGCCTCAAC CAGTGCATCT GAATCGGCAT CAACCAGTGC GTCACCTCAG	360
CAAGTACTAG TGCATCAGCT TCAGCATCAA CGAGTGCATC GGCTTCAGCA TCAACCAGTG	420
CATCAGAGTC AGCAAGTACG AGTGCCTCAC CCTCCGCATC AACAAAGTGC TCGGCTTCAG	480
CAAGTACTAG CGCCTCAGCC TCAGCGTCAA CAAGTGCCTG AGCTTCCGCG TCAACCAGCG	540
CCTCGGCCCTC AGCAAGTATC TCAGCGTCTG AATCGGCATC AACAAAGTGC TCGGCTTCAG	600
CATCAACGAG TGCATCAGTC TCAGCAAGCA CCAGTGCCTC GGCTCAGCA AGCACCAGCG	660
CGTCTGAATC CGCATCAACC AGTGCCTCAG CCTCAGCAAG TACCTCAGCA TCTGAATCAG	720
CATCAACAAG TGCATCGGCT TCAGCAAGCA CAAGTGCCTG AGCCTCAGCA AGTATCTCAG	780
CGTCTGAATC GGCATCAACG AGTGCCTCCG CCTCAGCAAG TACTAGCGCC TCAGCAGTCAG	840
CGTCAACAAG TGCTTCGGCT TCAGCGTCAA CGAGTGCCTC TGAGTCAGCA TCAACGAGTA	900
CGTCAGGCTC AGCAAGCACA TCAGCTTCTG AATCTGCATC AACCAAGTGC TCAAGCCTCAG	960
CATCGACAAG CGCCTCAGCT TCAGCAAGTA CCAGTGCCTC AGCCTCAGCA AGTACCAAGTG	1020
CTTCAGGCTC AGCGTCGACA AGTGCCTCCG GCTCAACCAG TGCATCTG	1068

(2) INFORMATION FOR SEQ ID NO: 374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

CAGCATCAAC GAGTGCTTCA GTTCAGCGT CAACCAAGTGC CTCTGAATCA GCTTCAACAA	60
GTGCCTCGGC TTCAAGCAAGC CCCAGTGCCTG CGGCTTCAGC AAGTACTAGT GCATCGGCTT	120
CAGCATCGAC AAGTGCCTCT GAATCGGCAT CAACGAGTGC TTGGCTTCA GCATCAACGA	180
GTGCCTCAGC CTCAGCAAGC ACATCAGCTT CTGAATCTGC ATCAACCAGT GCGTCCGTT	240

1388	
CAGCGTCAAC CAGTGCCTCG GCTTCAGCGT CGACAAGTGC TTTCGGCTTCA GCATCAACGA	300
GTGCGTCGGC CTCAGCAAGC GCAAGTACCT CAGCGTCAGC TTTCGGCTTCA ACCAGTGCCT	360
CGGCTTCAGC AAGCACAAGT GCGTCAGCCT CAGCGAAGTAT CTCAGCGTCT GAATCGGCAT	420
CAACGAGTGC GTCTGAGTCA GCATCAACGA GTACGTCAGC CTCAGCAAGC ACATCAGCTT	480
CTGAAATCTGC ATCAACCAGT GCGTCAGCCT CAGCGATCGAC AAGCGCCTCA GCTTCAGCAA	540
GTACCAGTGC TTCAGCCTCA GCGTCGACAA GTGCGTCGGC CTCAGCCTCA GCATCTGAAT	600
CGGCATCAAC CAGTGCCTCA	620

(2) INFORMATION FOR SEQ ID NO: 375:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 720 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

GTATTGGGGC GCCCCAACCT CTATGTGACT ACGGATTATT TCCTAGATTA CATGgGGATA	60
AACCATTAG AAGAATTACC AGTGATTGAT GAGCTTGAGA TTCAAGGCCA AGAAAGCCAA	120
TTATTTGGTG AAAGGATAGA AGAAGATGAG AATCAATAAG TATATTGCCA ACGCAGGTGT	180
GGCCAGTAGG AGAAAAGCAG AAGAGCTGAT TAAGCAAGGC TTGCTGACGG TTAACGGCCA	240
AGTGGTGCCT GAACTAGCAA CCACTATCAA GTCAGGCGAC AAGGTCGAAG TTGAAGGTCA	300
ACCTATCTAC AACGAAGAAA AGGTCTACTA TCTGCTTAAC AAACCACGCG GTGTGATTT	360
CAGTGTGACA GATGATAAGG GTCCCAAGAC GGTGTCGAC CTCTTGCCCA ATGTCAAAGA	420
GCGTATTTAC CCTGTGGGTC GTTTGGACTG GGATACATCA GGTGCTTGA TTTTGACCAA	480
TGATGGGGAC TTTACAGACG AGATGATTCA CCCTCGTAAT GAGATTGACA AGGTTTATGT	540
CGCGCGTGTAA AGAGGTGTGG CCAATAAGGA CAATCTCCGC CCCTTGACCC GTGGTCTTGA	600
GATTGATGGT AAGAAAACCA AGCCATAATA TATAGGTTTT GTAGCCTCTA CACCATAAAT	660
ATTTGCTAAT AAAATACTG TATTATTACC CTCTTAAGGT GCGAAATTAT TCAAGTTCTT	720

(2) INFORMATION FOR SEQ ID NO: 376:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 648 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

1389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

CGCCATTTCC	CATCGTACCG	CCGAAATCC	CAGCGCCTCA	GCCATCAAAT	ATCCTATCAA	60
CGTTCTCAAA	AAAAGTGACC	GCTCTCTCAT	CATGTTCCA	AGTGGTAGCC	GCCACTCAA	120
CGATGTCAAG	GGGGCGCAC	ACTskATTGC	CAAAATGGCC	AAGGTCCGTA	TCATGCCGGT	180
TACCTACACC	GGTCCCAGTA	CTTTGAAGGG	CTTGATTAGC	CGTGAACGTG	TCGATATGAA	240
CTTTGGAAAT	CCAATCGATA	TCTCAGATAT	CAAGAAAATG	AATGATGAAG	GCATTGAAAC	300
AGTCGCCAAT	CGTATTCAA	CAGAATTCCA	ACGCTGGAC	GAAGAAACGA	AACAATGGCA	360
CAATGATAAA	AAACCAAATC	CACTCTGGTG	GTTTATCCGC	ATCCCTGCC	TCATCCTTGC	420
TATTATCCTC	GCTATCCTAA	CCATCATCTT	TAGCTTATC	GCAAGCTTCA	TCTGGAACCC	480
AGATAAGAAA	AGAGAAGAAC	TTGCATAGAA	GAAATGAACC	TTGGCCAAAC	AGCTAAGGTT	540
TTCATTTATA	TAGTAGATTG	GwACTAGAAAT	AGTACACCTC	TACTTCTAAA	ACATTTTAG	600
AAATCGATTT	GACTGTCCTG	ATCGATTTGT	CCTAATCTTA	TTTCAATT		648

(2) INFORMATION FOR SEQ ID NO: 377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 690 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

GTGCATCGCT	TTCAGCATCG	ACAAGTGCCT	CTGAATCGGC	ATCAACGAGT	GCTTCGGCTT	60
CAGCATCAAC	GAGTGCCTCA	GCTTCAGCAA	GCACATCAGC	TTCTGAATCT	GCATCAACCA	120
GTGCGTCCGC	TTCAGCGTCA	ACCAGTGCCT	CGGCTTCAGC	GTCGACAAGT	GCTTCGGCTT	180
CAGCATCAAC	GAGTGCCTCG	GCCTCAGCAA	GCGCAAGTAC	CTCAGCGTCA	GCTTCCGCCT	240
CAACCAAGTGC	GTCCGCTTCA	GCAAGCACA	GTGGCGTCAGC	CTCAGCAAGT	ATCTCAGCGT	300
CTGAATCGGC	ATCAACGAGT	GCGTCGGCCT	CAGCAAGCGC	AAGTACCTCA	GCGTCAGCTT	360
CCGCCTCAAC	CAGTGCCTCG	GCTTCAGCAA	GCACAAGTCC	GTCAGCCTCA	GCAAGTATCT	420
CAGCGCTCTGA	ATCGGCATCA	ACGAGTGCCT	CTGAGTCAGC	ATCAACGAGT	ACGTCAGCCT	480
CAGCAAGCAC	ATCAGCTTCT	GAATCGGCAT	CAACCAGTGC	GTCAGCCTCA	GCATCGACAA	540
GCGCCTCAGC	TTCAGCAAGT	ACCAAGTGCCT	CAGCCTCAGC	GTCGACAAGT	GCGTCGGCCT	600
CAACCAGTGC	ATCTGAATCG	GCATCAACCA	GTGCCTCAGC	CTCAGCAAGT	ACTAGTGCAT	660

1390
CAGCTTCAGC ATCAACGAGT GCATCGGCTT 690

(2) INFORMATION FOR SEQ ID NO: 378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1003 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

CGAGATTCTC TGGAGTTATG GATGTCGTTCA	60
AAATATGTGC ACGTTGGAAT GTTAGTGCTT	
ATATGGGGGG AACAGAACATCC TCTCTTGATT	120
GAAGACAAGC TAGTCATTAG GCTGGTTTGT	
CTTTTTGTCA ACTGTAGTGG GTTGATATAA TAGTATTAGT	180
GAGTGGGATA AAAGTTTCAT	
TTAGTTTATT CAGTACAAAT TTAACGGGTC AAGATTATAA TACTAGTGGT	240
GTGTTTGGG	
CTGAGAGAAG TATCTTGATT TTATGTGTGG TTTTTATACT TACAGTTGTT	300
CTGCTCCAAA	
GAGCTTGTAG AGAAGAATTA GCTCATAAAG GAGATTGATT ATTTTGATAT	360
CAAAAGGATG	
CACAGGATAA CCTGATGCAT TTTTTAGCG ACAAATGCTTG CTACTTCCTT	420
CTGTCGAATT	
TAGACAATTT TAAACCCCAA TTATTCCACCC CAAATCTAAA AACCATCCAG	480
AATCCCTTGCC	
TTAGCTTACA	
TTCTGGATGG TTTCTTTTTT CACCCAATGG GTGTTTTTA CTAGACAAAA	540
540	
AAGAGTTTCC CTTTTATGGT ATAAGTGTAG AAAAAAACAC AAAAGAAAG GAAACTCACA	600
TGAACAGTTT ACCAAATCAT CACTTCCAAA ACAAGTCTTT TTACCAACTA	660
TCTTTCGATG	
GAGGTCATTT AACCCAGTAT GGTGGTCTTA TCTTTTTCA GGAACTTTTT	720
TCCCAGTTGA	
AACTAAAAGA CGGGATTCT AAGTATTTAG TAACGAATGA CCAACGCCGC TACTGTCGTT	780
780	
ATTGGGATTTC AGATATCCTT GTCCAGTTCC TCTTCAACT GTTAACAGGT TATGGAACGG	840
ACTATGCTTG TAAAGAATTG TCAGCTGATG CCTACTTTCC AAAATTATTG	900
GAAGGAGGGC	
AGCTTGCTTC ACAGCCAACC TTATCCCGTT TTCTTTCCAG AACTGACGAG GAAACAGTCC	960
ATAGTTGCG ATGCCCTAAC CTTGAATTGG TCGAATTCTT TTT	1003

(2) INFORMATION FOR SEQ ID NO: 379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 738 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

1391

CCGATGATTC TGATTGGTTT GCTCTTTACT TTGCTGGAA TTTTGAGGTA GATCTATGAT	60
TGAAATACTA ATTGTTTAG CTATTATCCT ATCTCTTGCT TTGATTGTAT TGGTAACTAT	120
ACAAACCCGT CAAATCAAC TATTTCCAT GGATGCCACT AGTAATATTG GTAAACCAAG	180
CTACTGGCAG AGCAACACCT TGGTCAAGGT GCTCACTTA TTGGTGAGTT TGCTTTATT	240
TATTCTACTA TTAACCTTTA TGGTGATTAC TTATAAATAA AAGAAAACCTT CAGATATTCA	300
CCTTTTGTTG ATTGGTCTGA AGTTTTCTTT TTTTACTCA ATGAAAATCA AAGAGCAAAC	360
TAGGAAGCTA GCCGCACkGC TCAAAACACC GTTTGAGGT TGTAGATATA ACTGACGAGC	420
GACTCAAAAC ACCGTTTGA GGTTGTAGAT ATAACGTACG AGCAGCTCAA AACACCGTTT	480
TGAGGTTGTG GATAGAACTG ACGAGGACT CAAAACACCG TTTTGAGGTT GTGGATAGAA	540
CTGACGAAAGT CGcTCAAAAC ACCGTTTGA GGTTGTGGAT AGAACTGACG AAtgctCAA	600
ACACCGTTT GAGGTTGTGG ATAGAACTGA CGAAGCgaaC ATATATACAG CAAGGGCAGC	660
CTGACGTGGT TTGAAGAGTA TTACTGTCTA TATTTTGTT AAAATCAAC TTTTACTTGG	720
ATGAAGGTTT TTTTTTTT	738

(2) INFORMATION FOR SEQ ID NO: 380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 695 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

CCGTCTTATC AAAGAGGTTA ACAAAGGCAC CAAATTTCTC GATACGAACG ACTTTAGCAC	60
GGTAAACTTC ATCCACTTTG GCTTCACGAA CCAAAACCGAC AATAATTTCT TTGGCACGGT	120
TAATAGCATC TTGGTCACTA GAGTAGATAG ACACATTTC TTCTTCGTCT ATATCAATCT	180
TAACACCTGT TTCAGCGATA ATCTTGTGCA TGGTTCTCC ACCCTTACCG ATGACAATCT	240
TAATCTTGTC CACATCAATC TTGATCGTAT CAATTTCGG AGCAGTTGGA GCCAATTCTG	300
GACGAACTTC TGGAAATGGTT GCTTCATGA CATCAAGGAT TTCAAAACGC GCTTTCTTGG	360
CTTGAGCAAG AGCCTCCGTC AAGATTCTG CAGTAATCCC TTGAATCTTG ATATCCATT	420
GAAGGGCTGT AATCCCATCA CGAGTACCTG CAACCTTGAA GTCCATATCT CCAAAGTGAT	480
CTTCCAAACC TTGGATATCT GTCAATACTG TGTAGTTATT TCCATCTGAG ATAAGCCCCA	540
TAGCAATACC AGCTACTGGC GCCTTGATTG GCACACCACC AGCCATAAGG GCAAGAGTTC	600

CCGCACAGAT AGAAGCTTGA GATGAAGAAC CGTTTGATTC CAAAACCTCT GCTACTAGAC	1392	660
GGATAGCGTA GGGGAATTCT TCCAAGCTTG GCAGG		695

(2) INFORMATION FOR SEQ ID NO: 381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 691 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

GACATCTTAT CTAAATACAT GCTAATATAT TTAGATACAA ACATTCCAAC TTGATAATTT	60
TCACTCATCT TTCATCATTC CTTATACAAC TATGCAGTAT AAATAGAATA GTTTTCTCAT	120
CAGAATGAGA CTATTTAAT ATTAGATCCC CAATTATTCA CCCCCAATCT AAAAACCATC	180
CAGAACCTT GCCTTAGCTT AGATCCTGGA TGTTTCTTT TTTCACCCAA TGGGTGTTT	240
TTACTAGACA AAAAGAGTT TCCCCTTAT GGATAAGTG TAGAAAAAAA CACAAAAAGA	300
AAGGAAACTC ACATGAACAG TTTACCAAAT CATCACTTCC AAAACAAGTC TTTTTACCAA	360
CTATCTTCG ATGGAGGTCA TTTAACCCAG TATGGTGGTC TTATCTTTT TCAGGAACCTT	420
TTTTCCCACT TGAAACTAAA AGACGGGATT TCTAAGTATT TAGTAACGAA TGACCAACGC	480
CGCTACTGTC GTTATTCGGA TTCAGATATC CTTGTCCAGT TCCTCTTCA ACTGTTAACCA	540
GGTTATGGAA CGGACTATGC TTGTAAGAA TTGTCAGCTG ATGCCTACTT TCCAAAATTG	600
TTGGAAGGAG GGCACCTTGC TTCACAGCCA ACCTTATCCC GwTTTCTTTC CAGAACTGAC	660
GAGGAAACAG TCCATAGTTT GCGATGCCCTC A	691

(2) INFORMATION FOR SEQ ID NO: 382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

ATCTCTCTGC GTAATGGTCC TCAGATAACT CTGATGATGT GTGGCGATAT AGAACTGAGC	60
CAAGTTATGC CTAAAGGCC TTAGGAATAG GAGCTTTCAC AAGCTTATCC AGATGATTAT	120
CTTTTACTCG TTATGGACAA TGCTATATGG CATAAAATCAA GTACCTTAAA GATTCCGACT	180
AATATTGGCT TTGCATTTAT TCCTCCATAC ACACCAAGAGA TGAACCCAT TGAACAAGTG	240

1393

TGGAAAGAGA TTCGTAACG TGGATTTAAG AATAAAGCCT TTGAACTTT GGAAGATGTC	300
ATACAAGGAC TGGAGAAGGA GGTGATAAG TCCATCGTTA ATCGGAGACG GACTAGAATG	360
CTTTTGAAA ACAGATGAGT ATAAAAAGAA AGTCCTCATT TCAATAGAAA TCACGACTTT	420
CTGATGAATT TATAGTAAAA TGAAATAAGA ACAGGGATAGT CAAATCGATT TCTAACAAATG	480
TTTTAGAAGC AGAGGTGTAC TATTCTAGTT TAAATCCACT ATATTTGGGG AGTGTAGAAGA	540
AAGCCCTTCA TCAGCCAATC TACTTGTCA GGTGCGAGAG CTTTGACATC CTTTCTGTA	600
CTGGACCAAG TCAGTTTCC GTTCTCAAAG CGTTTATATA ATATCCAAA TCCTTGACCA	660
TCCCAGTAAA GAACTTTAAA GCGGCTTTA CGTCCACAC AAAAGAGAAA GACTTGATCG	720
GAGAAAGGAT CCAATTCAA GTGGGTTTGG	750

(2) INFORMATION FOR SEQ ID NO: 383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 738 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

TCAAATTCTT CGGGTCCGC ATATCTnTCT TCGTACACGG CAGTCACTTG GTCTTCACT	60
ACTCGAGTCG CAGCTTCACG GGCAATTTC TCTTCTACTT GAACTGCCTT TTGGAGGTCA	120
CTGTTGTTAGG CTGCAATGAT TTCAGCTTGC AATTCAAGCAT CCACGTGAAG CAATTCCACT	180
TCTGCTTTT CTTTACCGAC AGCAGCAACG ATTTCTTCTT GGAAGGCAAT CAATTCTTG	240
ACAGCTTCGT GCCCTTAAAG GAGCGCTTCC AACATGATTT CTTCTGACAA TTCTTGGCA	300
CCAGACTCTA CCATGTTGAT AGCGTCTTGC GTTCCAGCTA CTGTCAATTG AAGAAGAGAT	360
TGCTCTGCTT GTTCTTGACT TGGGTTGATG ATGATTTGGC CATCTACATA TCCCACCTGT	420
ACCCCAGCAA TTGGTCCGTC AAATGGAATA TCTGAAATAG ACAGTGCCAA AGATGAACCA	480
AAACATAGCAG CCATTGGTGC AGATGCATTT TCATCATAAG AAAGCACTGT ATTGATGACT	540
TGGACTTCAT TACGGAAACC TTCCGAAAC ATAGGACGAA TCGGACGGTC AATCAAACGC	600
GCTGTCAAGG TCGCATCTGT TGAAGGACGT CCTTCACGTT TCATAAAGCC ACCAGGAAAC	660
TTCCCAGCCG CATACTTTT TTCTTCGTAG TTGACTTGGG GTGGGAAGAA ATCCTCAGTT	720
GCCATTCTTCTT GGGGATCC	738

(2) INFORMATION FOR SEQ ID NO: 384:

1394

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 657 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

CCCCCTATTT	ACCGTGGACT	AAAGTTGTAC	AAGAAAAGTG	CAAATAAGAA	ATCTCCAGAT	60
TAGGAACATAT	ATATGAGTTC	TCTAGTCTGG	AGATTTTC	ATAGACTTCG	TTATTGGGCG	120
GTTACTTTCG	AAACTTTGAA	AACTTCAAAA	AACGGATTTT	TATCGCTTTC	AAATTCTTTT	180
GGGGTCAAAC	TCAGTAACCT	ATTGCCTTG	TAGACTTCAT	GACGCTCAGG	GTATACTTTC	240
AAGGTCCCAA	ATAGCCAAGA	ATCGTCAGCG	ATATTATCTG	AATCATCTCC	TTCTTGTCT	300
CCTTTAGTTC	GCCTGAGGAC	AGCCCTGACA	CGCGCCAGAA	TTCTCTAGGG	CTAAAAGGCT	360
TGGTCAGGTA	GTCATCAGCC	CCTAATTCCA	AGGCCAAAC	CTTATCAAAT	TCATCACTTT	420
TCGCAGAAAC	CATCATAATT	GGAGTTTGAA	CGCCCTTGGC	TCTCAGCCGC	TTACAAACTT	480
CCATGCCATC	TAATTGTGGT	AACATGATAT	CAAGCAAGAT	AAAATCAAAG	GGTTCTGTPT	540
CTGCCAAAGC	TAAGGCCATTC	CGTCCATTG	TCACCAATTG	AGTAGAAAAG	CCTTCCTTAC	600
TTAAATGGTA	GTCAAGUAAT	TTCAAGAATGT	GTTCATC	ATCCACTAAT	AAGACTT	657

(2) INFORMATION FOR SEQ ID NO: 385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 586 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

CCGCATCAGC	ATCAACGAGT	GCATCGGCTT	CACGTCAACC	AGTGCATCAG	TCTCAGCAAG	60
CACCAAGTGC	TCGGCTTCAG	CATCAACGAG	TGCCTCAGCC	TCAGCAAGTA	TCTCAGCGTC	120
TGAATCGGCA	TCAACGAGTG	CGTCAGCTCA	GCAAGTACTA	GTGCATCGGC	TTCAGCAAGC	180
ACCAGTGCCT	CGGCTTCAGC	ATCAACCAGT	GCCTCAGCCT	CAGCAAGTAT	CTCAGCGTCT	240
GAATCGGCAT	CAACGAGTGC	GTCACTTCAG	CAAGTACTAG	TGCATCAGCA	TCAGCATCAA	300
CGAGTGCATC	GGCTTCAGCA	AGTACCAAGCG	CCTCAGCTTC	AGCAAGCACC	AGTGCCTCAC	360
CTCAGCAAGT	ACCAGCGCCT	CAGCCTCAGC	AAGCACCAGT	GCCTCAGCTT	CAGCAAGTAC	420
CAGTGCCTCA	CCTCAGCATC	GACAAGTGCG	TCGGCTTCAG	CAAGTACCTC	AGCGTCTGAA	480

1395

TCAGCATCAA CGAGTGGTC AGCTTCAGCA TCAACCAGTG CCTCAGCCTC AGCAAGTATC	540
AGTGCCTCAG CTTCAGCATC AACGAGTGGC TCAGCTGCAG CAAAGTA	586

(2) INFORMATION FOR SEQ ID NO: 386:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 451 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

CGTCGGCTTC AGCATCAACG AGTGCATCAG CTTCAGCATC ACAAGTGCT TCAGCTTCAG	60
CAAGTACAG TCGCTCGCT TCAGCATCAA CGAGTGCTTC AGTCTCAGCG TCAACCAGTG	120
CCTCTGAATC CGCATCAACA AGTGCCCTCGG CTTCAGCAAG CACCAGTGCT TCGGCTTCAG	180
CGTCAACGAG TGCCTCTGAG TCAGCATCAA CGAGTGGTC ACCTCAGCAA GCACATCAGC	240
TTCTGAATCT GCATCAACCA GTGGCTCAGC TTCCCATCA ACAAGCGCCT CGGCCTCAGC	300
AAAGTACAAGT GCTTCAGCCT CAGCATCAAC CAGTGCATCA GCTTCAGCCT CAACAAGTGC	360
TTCAGCCTCA GCGTCAACCA GTGCCCTGGC TTCAAGCAAGT ACCAGTGCAGT CAGTTcAGCA	420
AGCACAAAGTG CGTCAATTAA GCATCAACCA G	451

(2) INFORMATION FOR SEQ ID NO: 387:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 425 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

TCTCAGCAAG CACCATGGCG TCGGCTTCAT CAAGCACAG CGCGTTGAA TCCGCATCAA	60
CCAGTGCTTC AGCTTCAGCC AAGTTACCTC AGCATCTGAA TCAGCATCAA CAAGTGCATC	120
GGCTTCAGCA AGCACAAAGTG CTTCAGCTCA GCAAGTATCT CAGCGTCTGA ATCGGCATCA	180
ACGAGTGCAGT CGCGCTTCAGC AAGTACTAGC GCCTCAGCAT CAGCGTCAAC AAGTGCTTCG	240
GCTTCAGCGT CAACGAGTGC GTCTGAGTCA GCATCAACGA GTACGTCAGC CTCAGCAAGC	300
ACATCAGCTT CTGAATCTGC ATCAACCAGT GCGTCAGCCT CAGCATCGAC AACCGCCTCA	360
GCTTCAGCAA GTACCAAGTGC GTCAGCCTCA GCAAGTACCA GTGCTTCAGC CTCAGCGTCG	420

1396

ACAAG

425

(2) INFORMATION FOR SEQ ID NO: 388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

AGAGGATCCC CGGATCCTCA GTCGCTGAGA	60
TAACTCCTTT GGGCTTGTTC ATCATGTAGT	
AGACAAACTC TTCATACTCC AACACTTGC CATTATGC	120
GAATCTCATC TATTTTTCT	
TTTTTTGCA ATTTAGCTGA TTTTCTTTT TTACCATTTA	180
CAGTCACGCG CCCAGCCTG	
AGCAAGTTT TGACCTCAGT CCGACTTCCC ACCGCACAGG	240
CAACTAAAAAA TTTATCTAAT	
CTCATAGAAC TATTATATCA TATCAAAAGG AGGCTAGTAC	300
AATGACCAAC CTCCTTTCG	
TTTCATACTC TTCAAAATC TCTTCAAACG GCGTCAACGT	360
CGCCTTGCCG TATATATGTT	
ACTGACTTCG TCAGTTCTAT CTGCAACCTC AAAACAGTGT	420
TTTGAGCTGA CTTCGTCAGT	
TCTATCTGCA ACCTCAAAGC AGTGTCTGA GCATCCTGCG	480
GCTAGTTCC KAGTGTGCTC	
TITGATTTWC ATTGAGTATC AGATTAGGA AATTAACCTC	540
CTCGKCTCCA AAAAAKAGCT	
AAAACAATCA AGGCTCCTAA AATCGCTGGG AT	572

(2) INFORMATION FOR SEQ ID NO: 389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

CAACAAGTGC CTCGGCTTCA GCATGCACAA GTGCTTCAGC	60
TTCAGCATGT ACCTGAGCGT	
CTGAATCAGC ATCAACGTGT GCGTCCGCTT CAGCATGTAC	120
TGCTGCCTCA GCATCAGCGT	
CAACAwGTGC TTCGGCTTCA GCGTCAACGA GTGCGTCTGA	180
GTCAGCATCA ACGAGTACGT	
CAGCCTCAGC AAGCACATCA GCTTCTGAAT CTGCATCAAC	240
CAGTGCCTCA GCCTCAGCAT	
CGACAAGCGC CTCAGCTTCA GCAAGTACCA GTGCGTCAGC	300
CTCAGCAAGT ACCAGTGCTT	
CAGCCTCAGC GTCGACAAGT GCGTCGGCCT CAACCAAGTGC	360
ATCTGAATCG GCATCAACCA	
GTGCGTCAGC CTCAGCAAGT ACTAGCGCCT CAGCCTCAGC	420
ATCAACGAGT GCGTCCGCTT	

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CAGCAAGTAC TAGTCATCA GCATCAGCAT CAACGAGTGC ATCGGCTTCA GCAAGTACCA	480
GCGCCTCAGC TTCAGCAAGC ACCGG	505

(2) INFORMATION FOR SEQ ID NO: 390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

GCTAAGACTA CCTCATTAGG GGCACTAGGCT GCTAAAATAA CTGCAGCTGT GGTTAATGAC	60
AATACTGTAC TTTTTTTCAT TTTAATTCCCT TACATATTAA TATAACTTCC AATAGATAAT	120
AAACTTTAAC TTTGCTAGCC TTTGTTATAA AAAGTTTAC TAAGTATTAT CTAGGAAATA	180
GAGTAGTACA TTTATATATA ATTGTTATCT CTCTATAAAA ACAGTATATC ATTTAAAAAA	240
ATTTAAGTCA AAAAAATTAA CATTAGTTAA TTTATTTTT AGCACACATT AAAAAATAAG	300
ATTAGTACTC AATGAAAATC AAAGAGCAAA CTAGGAAACT AGCCGCAGAT TGCTAAAAC	360
AGTGTGTTGA GGTTGTAGAT GGAATGACGT AGTCAGCTCA AAACACTGTT TTGAAGTTGT	420
GGATAGAACT GACGAAGTCG GTACCGA	447

(2) INFORMATION FOR SEQ ID NO: 391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

AGCACCTGTC GTTGAATTCT ACAACAAAAT GTTGTAAATAT TTTATTGAAT AAGATAGGCC	60
TTGATATTAA GCACTTTGGG ACGTTCTCCC TTAGTGCTTT TTTGATTTCT CTTAGTATCC	120
AGCTATAATC GTTGAGACAT AACTAGACCG ATATAGTCCA AAGTGTATATA GTAAAATGAA	180
CCAAAAATAG TACACAATGT GGTATAATCC TTTTATGGCA TATTCAATAG ATTTTCGTA	240
AAAAGTTCTC TCTTATTGTG AGCGAACAGG TAGTATAACA GAAGCATCAC ACGTTTCCA	300
AATCTCACGT AATACCATTT ATGGCTGGTT AAAGCTAAAA GAGAAAACAG GAGAGCTAAA	360
CCACCAAGTA TAGTGTATTG AATCTATAAC AGTACACCTT GGCTGCTAAA ATATTTCTAT	420

1398	
AAATTAATTT GACTTCCCTG ATAGAGATGT TCACATCTTA TTTCAAACTA CTATATAAGT	480
TCTATAATCT CTTTATAAAGA TTTGCCCATC AGACAAAATA GAACGATTTG AAGGCCTTTA	540
TGATATTTAG CTGTACGAGA GTCTTTAAA AG	572

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MISSING UPON TIME OF PUBLICATION

1400

DENMARK

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person approved by the applicant in the individual case.

SWEDEN

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PUT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant, any request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent Office or any person approved by the applicant in the individual case.

UNITED KINGDOM

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the International publication of the application.

NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapse, the microorganism shall be made available as provided in Rule 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever two dates occurs earlier.

SINGAPORE

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for international publication of the application.

NORWAY

The applicant hereby requests that, until the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

AUSTRALIA

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Registration), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

ICELAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the Icelandic Patent Office), or has been finally decided upon by the Icelandic Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected in the art.

What Is Claimed Is:

- 25 1. Computer readable medium having recorded thereon the nucleotide sequence depicted in SEQ ID NOS:1-391, a representative fragment thereof or a nucleotide sequence at least 95% identical to a nucleotide sequence depicted in SEQ ID NOS:1-391.
- 30 2. Computer readable medium having recorded thereon any one of the fragments of SEQ ID NOS:1-391 depicted in Tables 2 and 3 or a degenerate variant thereof.
- 35 3. The computer readable medium of claim 1, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.
- 40 4. The computer readable medium of claim 3, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.
- 45 5. A computer-based system for identifying fragments of the *Streptococcus pneumoniae* genome of commercial importance comprising the following elements:
 - a) a data storage means comprising the nucleotide sequence of SEQ ID NOS:1-391, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS:1-391;
 - b) search means for comparing a target sequence to the nucleotide sequence of the data storage means of step (a) to identify homologous sequence(s), and
 - c) retrieval means for obtaining said homologous sequence(s) of step (b).
- 50 6. A method for identifying commercially important nucleic acid fragments of the *Streptococcus pneumoniae* genome comprising the step of comparing a database comprising the nucleotide sequences depicted in SEQ ID NOS:1-391, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS:1-391 with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence is not randomly selected.

60 7. A method for identifying an expression modulating fragment of
Streptococcus pneumoniae genome comprising the step of comparing a database
comprising the nucleotide sequences depicted in SEQ ID NOS:1-391, a
representative fragment thereof, or a nucleotide sequence at least 95% identical to
the nucleotide sequence of SEQ ID NOS:1-391 with a target sequence to obtain a
nucleic acid molecule comprised of a complementary nucleotide sequence to said
target sequence, wherein said target sequence comprises sequences known to
65 regulate gene expression.

70 8. An isolated protein-encoding nucleic acid fragment of the *Streptococcus*
pneumoniae genome, wherein said fragment consists of the nucleotide sequence of
any one of the fragments of SEQ ID NOS:1-391 depicted in Tables 2 and 3, or a
degenerate variant thereof.

75 9. A vector comprising any one of the fragments of the *Streptococcus*
pneumoniae genome SEQ ID NOS:1-391 depicted in Tables 2 and 3 or a
degenerate variant thereof.

80 10. An isolated fragment of the *Streptococcus pneumoniae* genome,
wherein said fragment modulates the expression of an operably linked open reading
frame, wherein said fragment consists of the nucleotide sequence from about 10 to
200 bases in length which is 5' to any one of the open reading frames depicted in
Tables 2 and 3 or a degenerate variant thereof.

85 11. A vector comprising any one of the fragments of the *Streptococcus*
pneumoniae genome of claim 8.

12. An organism which has been altered to contain any one of the
fragments of the *Streptococcus pneumoniae* genome of claim 8.

90 13. An organism which has been altered to contain any one of the
fragments of the *Streptococcus pneumoniae* genome of claim 10.

95

14. A method for regulating the expression of a nucleic acid molecule comprising the step of covalently attaching to said nucleic acid molecule a nucleic acid molecule consisting of the nucleotide sequence from about 10 to 100 bases 5' to any one of the fragments of the *Streptococcus pneumoniae* genome depicted in SEQ ID NOS:1-391 and Tables 2 and 3 or a degenerate variant thereof.

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15. An isolated nucleic acid molecule encoding a homolog of any of the fragments of the *Streptococcus pneumoniae* genome of SEQ ID NOS:1-391 and Tables 2 and 3, wherein said nucleic acid molecule is produced by a process comprising steps of:

105

- a) screening a genomic DNA library using as a probe a target sequence defined by any of SEQ ID NOS:1-391 and Tables 2 and 3, including fragments thereof;
- b) identifying members of said library which contain sequences that hybridize to said target sequence; and
- c) isolating the nucleic acid molecules from said members identified in step (b).

110

16. An isolated DNA molecule encoding a homolog of any one of the fragments of the *Streptococcus pneumoniae* genome of SEQ ID NOS:1-391 and Tables 2 and 3, wherein said nucleic acid molecule is produced a process comprising steps of:

115

- a) isolating mRNA, DNA, or cDNA produced from an organism;
- b) amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from said fragment of said *Streptococcus pneumoniae* genome to prime said amplification;
- c) isolating said amplified sequences produced in step (b).

120

17. An isolated polypeptide encoded by any of the fragments of the *Streptococcus pneumoniae* genome of SEQ ID NOS:1-391 and depicted in Table 2 and 3 or by a degenerate variant of said fragments.

125

18. An isolated polynucleotide molecule encoding any one of the polypeptides of claim 17.

19. An antibody which selectively binds to any one of the polypeptides of
claim 17.

130

20. A method for producing a polypeptide in a host cell comprising the
steps of:

135 a) incubating a host containing a heterologous nucleic acid molecule whose
nucleotide sequence consists of any one of the fragments of the *Streptococcus*
pneumoniae genome of SEQ ID NOS:1-391 and depicted in Tables 2 and 3, under
conditions where said heterologous nucleic acid molecule is expressed to produce
said protein, and

b) isolating said protein.

Figure 1

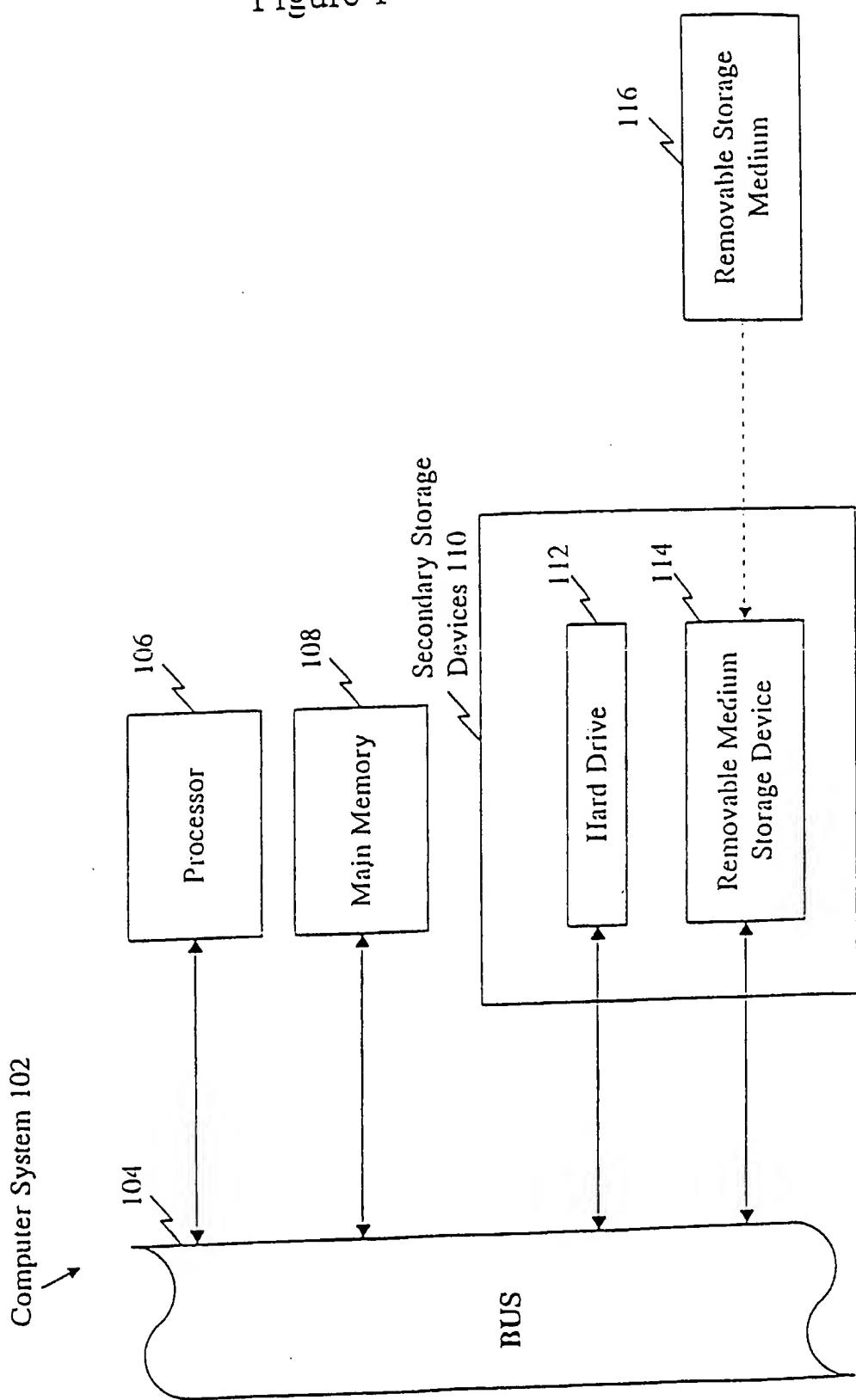
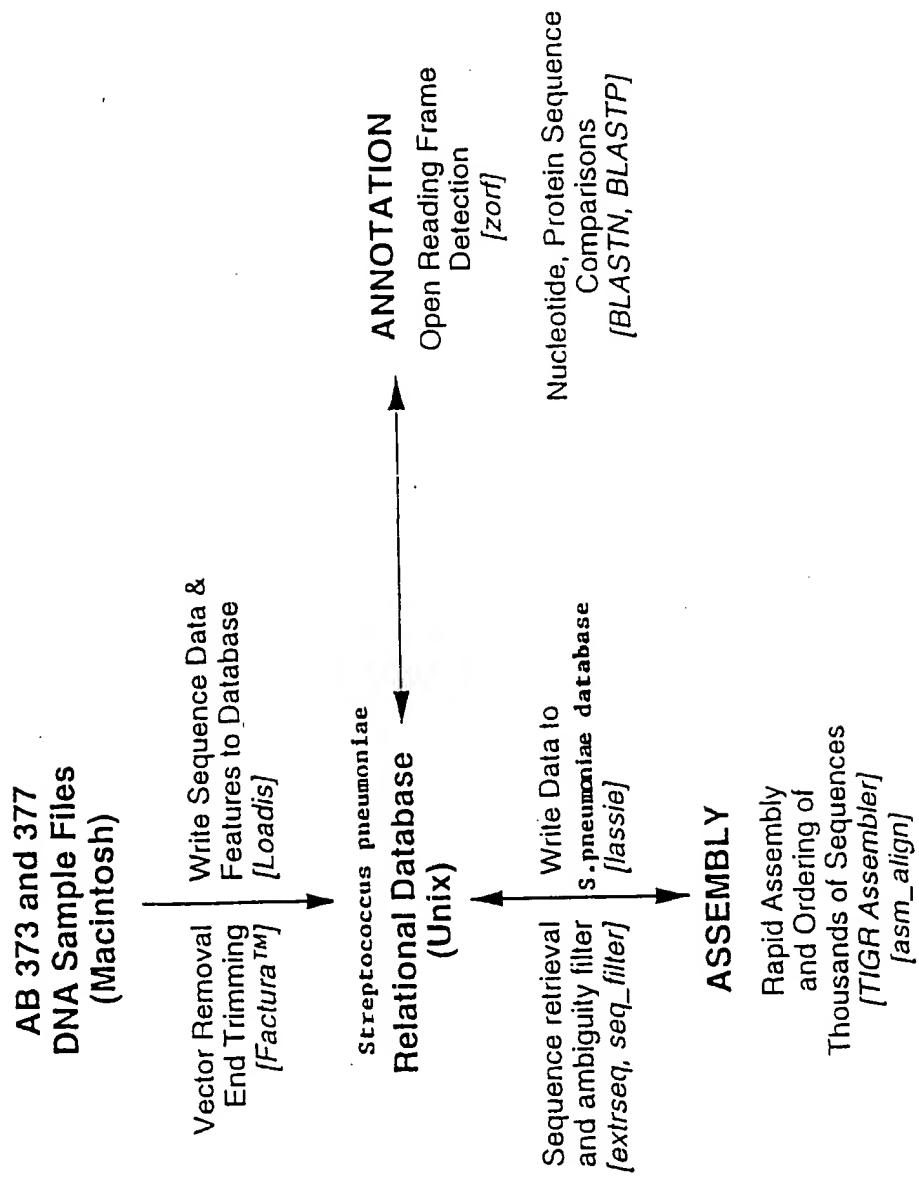


Figure 2



PCT

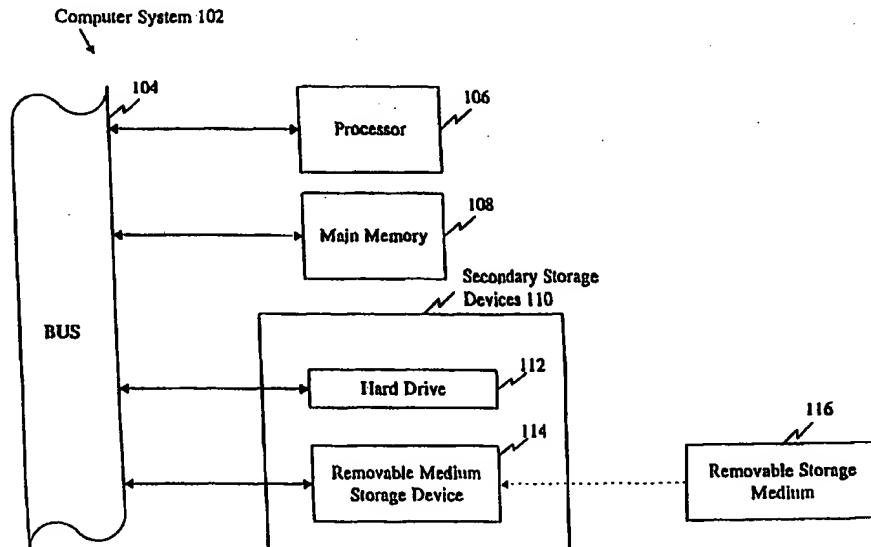
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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C12N 15/31, C07K 14/315, 16/12, C12Q 1/68	A3	(11) International Publication Number: WO 98/18931 (43) International Publication Date: 7 May 1998 (07.05.98)
(21) International Application Number: PCT/US97/19588		(74) Agents: BROOKES, A., Anders et al.; Human Genome Sciences, Inc., 9410 Key West Avenue, Rockville, MD 20850 (US).
(22) International Filing Date: 30 October 1997 (30.10.97)		
(30) Priority Data: 60/029,960 31 October 1996 (31.10.96) US		(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).
(71) Applicant (for all designated States except US): HUMAN GENOME SCIENCES, INC. [US/US]; 9410 Key West Avenue, Rockville, MD 20850 (US).		
(72) Inventors; and		
(75) Inventors/Applicants (for US only): KUNSCH, Charles, A. [US/US]; 2398B Dunwoody Crossing, Atlanta, GA 30338 (US). CHOI, Gil, H. [KR/US]; 11429 Potomac Oaks Drive, Rockville, MD 20850 (US). DILLON, Patrick, J. [US/US]; 1055 Snipe Court, Carlsbad, CA 92009 (US). ROSEN, Craig, A. [US/US]; 22400 Rolling Hill Road, Laytonsville, MD 20882 (US). BARASH, Steven, C. [US/US]; 582 College Parkway #303, Rockville, MD 20850 (US). FANNON, Michael [US/US]; 13501 Rippling Brook Drive, Silver Spring, MD 20850 (US). DOUGHERTY, Brian, A. [US/US]; 708 Meadow Field Court, Mount Airy, MD 21771 (US).		
		(88) Date of publication of the international search report: 20 August 1998 (20.08.98)

(54) Title: **STREPTOCOCCUS PNEUMONIAE POLYNUCLEOTIDES AND SEQUENCES**



(57) Abstract

The present invention provides polynucleotide sequences of the genome of *Streptococcus pneumoniae*, polypeptide sequences encoded by the polynucleotide sequences, corresponding polynucleotides and polypeptides, vectors and hosts comprising the polynucleotides, and assays and other uses thereof. The present invention further provides polynucleotide and polypeptide sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use.

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INTERNATIONAL SEARCH REPORT

In. National Application No
PCT/US 97/19588A. CLASSIFICATION F SUBJECT MATTER
IPC 6 C12N15/31 C07K14/315 C07K16/12 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 6 C12N C07K C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 96 33276 A (HUMAN GENOME SCIENCES INC ;UNIV JOHNS HOPKINS (US)) 24 October 1996 see claims 1-7 ---	1-7
A	ALTSCHUL S F ET AL: "BASIL LOCAL ALIGNMENT SEARCH TOOL" JOURNAL OF MOLECULAR BIOLOGY, vol. 215, 1990, pages 403-410, XP000604562 cited in the application see the whole document --- -/-	1-7

 Further documents are listed in the continuation of box C. Patent family members are listed in annex.

° Special categories of cited documents :

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- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

- "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- "&" document member of the same patent family

4 Date of the actual completion of the international search

27 March 1998

Date of mailing of the international search report

08.07.98

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HORNIG H.

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 97/19588

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	W.R. PEARSON AND D.J. LIPMAN: "Improved tools for biological sequence comparison" PROC. NATL. ACAD. SCI., vol. 85, April 1988, NATL. ACAD. SCI., WASHINGTON, DC, US, pages 2444-2448, XP002060460 cited in the application see the whole document	1-7
A	WO 95 06732 A (UNIV ROCKEFELLER ;MASURE H ROBERT (US); PEARCE BARBARA J (US); TUO) 9 March 1995 see the whole document	1-7
A	WO 95 31548 A (UAB RESEARCH FOUNDATION ;YOTHER JANET (US); DILLARD JOSEPH P (US)) 23 November 1995 see the whole document	1-7
A	WO 95 14712 A (RES CORP TECHNOLOGIES INC) 1 June 1995 see the whole document	1-7
A	WO 96 05859 A (AMERICAN CYANAMID CO) 29 February 1996 see the whole document	1-7
A	WO 93 10238 A (US HEALTH) 27 May 1993 see the whole document	1-7
A	EP 0 687 688 A (UNIV OVIEDO ;UNIV LEICESTER (GB)) 20 December 1995 see the whole document	1-7
A	EP 0 622 081 A (UAB RESEARCH FOUNDATION) 2 November 1994 see the whole document	1-7

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 97/19588

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. Claims Nos.:

because they relate to subject matter not required to be searched by this Authority, namely:

Remark: Although claims 1-4 could be, at least partially be considered as a mere presentation of information Rule 39.1(v), and claims 5-7 at least partially as a computer program, Rule 39.1(vi)PCT, the search has been carried out as far as possible in our systematic documentation.

2. Claims Nos.:

because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. Claims Nos.:

because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see continuation-sheet

1. As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-7

Remark on Protest

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

1. Claims: 1-7

Computer readable medium having recorded thereon the nucleotide sequence depicted in SEQ ID nos. 1-391, a representative fragment thereof or a nucleotide sequence at least 95% identical to a nucleotide sequence depicted in SEQ ID nos. 1-391; a computer-based system for identifying fragments of the *Streptococcus pneumoniae* genome of commercial importance comprising: a) a data storage means comprising said nucleotide sequence(s); b) search means for comparing a target sequence to the nucleotide sequence of the data storage means of step (a) to identify homologous sequence(s), and c) retrieval means for obtaining said homologous sequence(s) of step (b); a method for identifying commercially important nucleic acid fragments of the *Streptococcus pneumoniae* genome comprising the step of comparing a database comprising said nucleotide sequence(s) with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence is not randomly selected; a method for identifying an expression modulating fragments of the *Streptococcus pneumoniae* genome comprising the step of comparing a database comprising said nucleotide sequence(s) with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence comprises sequences known to regulate gene expression;

2. Claims: (8-20) partially

An isolated protein-encoded nucleic acid fragment of the *Streptococcus pneumoniae* genome, wherein said fragment consists of the nucleotide sequence of the fragment of SEQ ID no.1 depicted in Tables 2 and 3, or a degenerate variant thereof; a vector comprising the fragment of the *Streptococcus pneumoniae* genome SEQ ID no.1; an isolated fragment of the *Streptococcus pneumoniae* genome, wherein said fragment modulates the expression of an operably linked open reading frame, wherein said fragment consists of the nucleotide sequence from about 10 to 200 bases in length which is 5' to any one of the open reading frame of SEQ ID no.1 depicted in Tables 2 and 3 or a degenerate variant thereof; a method for regulating the expression of a nucleic acid molecule comprising the step of covalently attaching to said nucleic acid molecule a nucleic acid molecule consisting of the nucleotide sequence from about 10 to 100 bases 5' to any one of the open reading frame of SEQ ID no.1 and Tables 2 and 3 or a degenerate variant thereof; an isolated nucleic acid molecule encoding a homolog of SEQ ID no.1; an isolated polypeptide encoded by SEQ ID no.1 and depicted in Table 2 and 3; an antibody which selectively binds to any one of said polypeptides, a method for producing a polypeptide in a host cell comprising a) incubating a host containing a heterologous nucleic acid

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

molecule whose nucleotide sequence consists of SEQ ID no.1 and depicted in Table 2 and 3, under conditions where said heterologous nucleic acid molecule is expressed to produce said protein, and b) isolating said protein;

3-392. Claims: (8-20) partially

Idem as subject 2 but limited to each of the sequences of SEQ ID no. 2 to 391;

For the sake of conciseness, the second subject matter is explicitly defined, the other subject matters are defined by analogy hereto.

INTERNATIONAL SEARCH REPORT

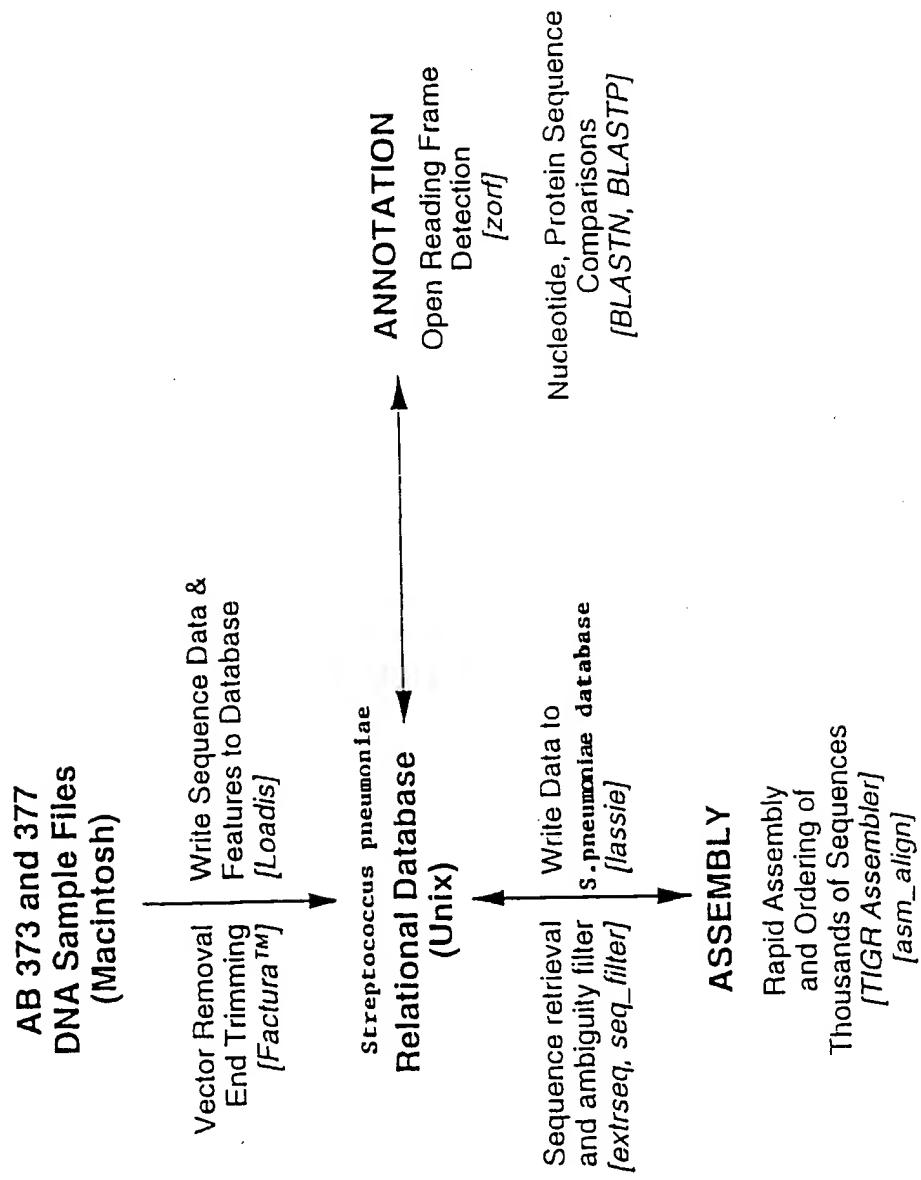
Information on patent family members

International Application No

PCT/US 97/19588

Patent document cited in search report	Publication date	Patent family member(s)		Publication date
WO 9633276 A	24-10-96	AU 5552396 A EP 0821737 A		07-11-96 04-02-98
WO 9506732 A	09-03-95	AU 7680994 A CA 2170726 A EP 0721506 A FI 960977 A JP 9504686 T NO 960839 A		22-03-95 09-03-95 17-07-96 30-04-96 13-05-97 19-04-96
WO 9531548 A	23-11-95	AU 2638595 A EP 0804582 A		05-12-95 05-11-97
WO 9514712 A	01-06-95	US 5474905 A		12-12-95
WO 9605859 A	29-02-96	US 5565204 A AU 3363695 A CA 2198251 A EP 0778781 A JP 10504717 T		15-10-96 14-03-96 29-02-96 18-06-97 12-05-98
WO 9310238 A	27-05-93	AU 3065892 A		15-06-93
EP 0687688 A	20-12-95	ES 2075803 A ES 2088820 A WO 9516711 A		01-10-95 16-09-96 22-06-95
EP 0622081 A	02-11-94	AU 682018 B AU 5769694 A CA 2116261 A FI 941695 A JP 7126291 A NO 941420 A US 5679768 A ZA 9401584 A		18-09-97 27-10-94 21-10-94 21-10-94 16-05-95 21-10-94 21-10-97 12-10-94

Figure 2



PCT

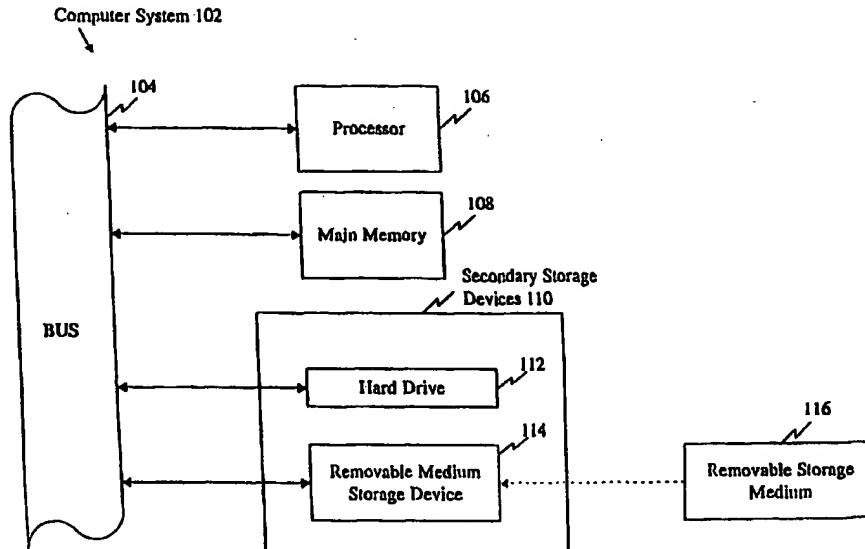
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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 6 : C12N 15/31, C07K 14/315, 16/12, C12Q 1/68		A3	(11) International Publication Number: WO 98/18931
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(30) Priority Data: 60/029,960 31 October 1996 (31.10.96) US		(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).	(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).
(71) Applicant (for all designated States except US): HUMAN GENOME SCIENCES, INC. [US/US]; 9410 Key West Avenue, Rockville, MD 20850 (US).		(88) Date of publication of the international search report: 20 August 1998 (20.08.98)	(88) Date of publication of the international search report: 20 August 1998 (20.08.98)
(72) Inventors; and (75) Inventors/Applicants (for US only): KUNSCH, Charles, A. [US/US]; 2398B Dunwoody Crossing, Atlanta, GA 30338 (US). CHOI, Gil, H. [KR/US]; 11429 Potomac Oaks Drive, Rockville, MD 20850 (US). DILLON, Patrick, J. [US/US]; 1055 Snipe Court, Carlsbad, CA 92009 (US). ROSEN, Craig, A. [US/US]; 22400 Rolling Hill Road, Laytonsville, MD 20882 (US). BARASH, Steven, C. [US/US]; 582 College Parkway #303, Rockville, MD 20850 (US). FANNON, Michael [US/US]; 13501 Rippling Brook Drive, Silver Spring, MD 20850 (US). DOUGHERTY, Brian, A. [US/US]; 708 Meadow Field Court, Mount Airy, MD 21771 (US).		(76) Published <i>With international search report. Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i>	(76) Published <i>With international search report. Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i>

(54) Title: **STREPTOCOCCUS PNEUMONIAE POLYNUCLEOTIDES AND SEQUENCES**



(57) Abstract

The present invention provides polynucleotide sequences of the genome of *Streptococcus pneumoniae*, polypeptide sequences encoded by the polynucleotide sequences, corresponding polynucleotides and polypeptides, vectors and hosts comprising the polynucleotides, and assays and other uses thereof. The present invention further provides polynucleotide and polypeptide sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use.

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INTERNATIONAL SEARCH REPORT

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According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 6 C12N C07K C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 96 33276 A (HUMAN GENOME SCIENCES INC ;UNIV JOHNS HOPKINS (US)) 24 October 1996 see claims 1-7 ---	1-7
A	ALTSCHUL S F ET AL: "BASIL LOCAL ALIGNMENT SEARCH TOOL" JOURNAL OF MOLECULAR BIOLOGY, vol. 215, 1990, pages 403-410, XP000604562 cited in the application see the whole document --- -/-	1-7

 Further documents are listed in the continuation of box C. Patent family members are listed in annex.

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- "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
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- "&" document member of the same patent family

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Date of the actual completion of the international search

27 March 1998

Date of mailing of the international search report

08.07.98

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HORNIG H.

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 97/19588

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	W.R. PEARSON AND D.J. LIPMAN: "Improved tools for biological sequence comparison" PROC. NATL. ACAD. SCI., vol. 85, April 1988, NATL. ACAD. SCI., WASHINGTON, DC, US; , pages 2444-2448, XP002060460 cited in the application see the whole document ---	1-7
A	WO 95 06732 A (UNIV ROCKEFELLER ;MASURE H ROBERT (US); PEARCE BARBARA J (US); TUO) 9 March 1995 see the whole document ---	1-7
A	WO 95 31548 A (UAB RESEARCH FOUNDATION ;YOTHER JANET (US); DILLARD JOSEPH P (US)) 23 November 1995 see the whole document ---	1-7
A	WO 95 14712 A (RES CORP TECHNOLOGIES INC) 1 June 1995 see the whole document ---	1-7
A	WO 96 05859 A (AMERICAN CYANAMID CO) 29 February 1996 see the whole document ---	1-7
A	WO 93 10238 A (US HEALTH) 27 May 1993 see the whole document ---	1-7
A	EP 0 687 688 A (UNIV OVIEDO ;UNIV LEICESTER (GB)) 20 December 1995 see the whole document ---	1-7
A	EP 0 622 081 A (UAB RESEARCH FOUNDATION) 2 November 1994 see the whole document -----	1-7

INTERNATIONAL SEARCH REPORT

...international application No.

PCT/US 97/ 19588

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. **Claims Nos.:**
because they relate to subject matter not required to be searched by this Authority, namely:
Remark: Although claims 1-4 could be, at least partially be considered as a mere presentation of information Rule 39.1(v), and claims 5-7 at least partially as a computer program, Rule 39.1(vi)PCT, the search has been carried out as far as possible in our systematic documentation.
2. **Claims Nos.:**
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. **Claims Nos.:**
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see continuation-sheet

1. As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-7**Remark on Protest**

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

1. Claims: 1-7

Computer readable medium having recorded thereon the nucleotide sequence depicted in SEQ ID nos. 1-391, a representative fragment thereof or a nucleotide sequence at least 95% identical to a nucleotide sequence depicted in SEQ ID nos. 1-391; a computer-based system for identifying fragments of the *Streptococcus pneumoniae* genome of commercial importance comprising: a) a data storage means comprising said nucleotide sequence(s); b) search means for comparing a target sequence to the nucleotide sequence of the data storage means of step (a) to identify homologous sequence(s), and c) retrieval means for obtaining said homologous sequence(s) of step (b); a method for identifying commercially important nucleic acid fragments of the *Streptococcus pneumoniae* genome comprising the step of comparing a database comprising said nucleotide sequence(s) with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence is not randomly selected; a method for identifying an expression modulating fragments of the *Streptococcus pneumoniae* genome comprising the step of comparing a database comprising said nucleotide sequence(s) with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence comprises sequences known to regulate gene expression;

2. Claims: (8-20) partially

An isolated protein-encoded nucleic acid fragment of the *Streptococcus pneumoniae* genome, wherein said fragment consists of the nucleotide sequence of the fragment of SEQ ID no.1 depicted in Tables 2 and 3, or a degenerate variant thereof; a vector comprising the fragment of the *Streptococcus pneumoniae* genome SEQ ID no.1; an isolated fragment of the *Streptococcus pneumoniae* genome, wherein said fragment modulates the expression of an operably linked open reading frame, wherein said fragment consists of the nucleotide sequence from about 10 to 200 bases in length which is 5' to any one of the open reading frame of SEQ ID no.1 depicted in Tables 2 and 3 or a degenerate variant thereof; a method for regulating the expression of a nucleic acid molecule comprising the step of covalently attaching to said nucleic acid molecule a nucleic acid molecule consisting of the nucleotide sequence from about 10 to 100 bases 5' to any one of the open reading frame of SEQ ID no.1 and Tables 2 and 3 or a degenerate variant thereof; an isolated nucleic acid molecule encoding a homolog of SEQ ID no.1; an isolated polypeptide encoded by SEQ ID no.1 and depicted in Table 2 and 3; an antibody which selectively binds to any one of said polypeptides, a method for producing a polypeptide in a host cell comprising a) incubating a host containing a heterologous nucleic acid

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

molecule whose nucleotide sequence consists of SEQ ID no.1 and depicted in Table 2 and 3, under conditions where said heterologous nucleic acid molecule is expressed to produce said protein, and b) isolating said protein;

3-392. Claims: (8-20) partially

Idem as subject 2 but limited to each of the sequences of SEQ ID no. 2 to 391;

For the sake of conciseness, the second subject matter is explicitly defined, the other subject matters are defined by analogy hereto.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

1. Claims: 1-7

Computer readable medium having recorded thereon the nucleotide sequence depicted in SEQ ID nos. 1-391, a representative fragment thereof or a nucleotide sequence at least 95% identical to a nucleotide sequence depicted in SEQ ID nos. 1-391; a computer-based system for identifying fragments of the *Streptococcus pneumoniae* genome of commercial importance comprising: a) a data storage means comprising said nucleotide sequence(s); b) search means for comparing a target sequence to the nucleotide sequence of the data storage means of step (a) to identify homologous sequence(s), and c) retrieval means for obtaining said homologous sequence(s) of step (b); a method for identifying commercially important nucleic acid fragments of the *Streptococcus pneumoniae* genome comprising the step of comparing a database comprising said nucleotide sequence(s) with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence is not randomly selected; a method for identifying an expression modulating fragments of the *Streptococcus pneumoniae* genome comprising the step of comparing a database comprising said nucleotide sequence(s) with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence comprises sequences known to regulate gene expression;

2. Claims: (8-20) partially

An isolated protein-encoded nucleic acid fragment of the *Streptococcus pneumoniae* genome, wherein said fragment consists of the nucleotide sequence of the fragment of SEQ ID no.1 depicted in Tables 2 and 3, or a degenerate variant thereof; a vector comprising the fragment of the *Streptococcus pneumoniae* genome SEQ ID no.1; an isolated fragment of the *Streptococcus pneumoniae* genome, wherein said fragment modulates the expression of an operably linked open reading frame, wherein said fragment consists of the nucleotide sequence from about 10 to 200 bases in length which is 5' to any one of the open reading frame of SEQ ID no.1 depicted in Tables 2 and 3 or a degenerate variant thereof; a method for regulating the expression of a nucleic acid molecule comprising the step of covalently attaching to said nucleic acid molecule a nucleic acid molecule consisting of the nucleotide sequence from about 10 to 100 bases 5' to any one of the open reading frame of SEQ ID no.1 and Tables 2 and 3 or a degenerate variant thereof; an isolated nucleic acid molecule encoding a homolog of SEQ ID no.1; an isolated polypeptide encoded by SEQ ID no.1 and depicted in Table 2 and 3; an antibody which selectively binds to any one of said polypeptides, a method for producing a polypeptide in a host cell comprising a) incubating a host containing a heterologous nucleic acid